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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:54 ; Search time 158.26 Seconds
(without alignments)
4.211 Million cell updates/sec

Title: US-09-723-197-5
Perfect score: 35
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 35 | 100.0 | 6 | 17 | AAR95666 | Angiotensin II fra |
| 2 | 35 | 100.0 | 6 | 19 | AAW65601 | Angiotensin II ana |
| 3 | 35 | 100.0 | 6 | 19 | AAW64732 | Angiotensin II pep |
| 4 | 35 | 100.0 | 6 | 19 | AAW71114 | Peptide AII(2-7) u |
| 5 | 35 | 100.0 | 6 | 19 | AAW65540 | Peptide motif havi |
| 6 | 35 | 100.0 | 6 | 20 | AAY49590 | Angiotensin analog |
| 7 | 35 | 100.0 | 6 | 20 | AAY33905 | Angiotensin II ana |
| 8 | 35 | 100.0 | 6 | 20 | AAY30543 | Amino acid sequenc |
| 9 | 35 | 100.0 | 6 | 20 | AAY30587 | Amino acid sequenc |
| 10 | 35 | 100.0 | 6 | 20 | AAY32718 | Angiotensin II ana |
| 11 | 35 | 100.0 | 6 | 20 | AAY33772 | Angiotensin II (AI |
| 12 | 35 | 100.0 | 6 | 20 | AAY15349 | Angiotensin II (AI |
| 13 | 35 | 100.0 | 6 | 20 | AAY15309 | Angiotensin II (AI |
| 14 | 35 | 100.0 | 6 | 21 | AAB27405 | Angiotensin II ana |
| 15 | 35 | 100.0 | 6 | 21 | AAB28103 | Angiotensin II ana |
| 16 | 35 | 100.0 | 6 | 21 | AAY84128 | Peptide comprising |
| 17 | 35 | 100.0 | 6 | 21 | AAY77041 | Angiotensin II (AI |
| 18 | 35 | 100.0 | 6 | 21 | AAY57405 | Angiotensin peptid |
| 19 | 35 | 100.0 | 6 | 22 | AAE08875 | AII peptide (resid |
| 20 | 35 | 100.0 | 6 | 22 | AAE02992 | Human angiotensin |
| 21 | 35 | 100.0 | 6 | 22 | AAE03155 | Human angiotensin |
| 22 | 35 | 100.0 | 6 | 22 | AAB91487 | Angiotensin peptid |
| 23 | 35 | 100.0 | 7 | 2 | AAP10431 | Angiotensin II oct |
| 24 | 35 | 100.0 | 7 | 16 | AAR87681 | Angiotensin III fo |
| 25 | 35 | 100.0 | 7 | 17 | AAR95665 | Angiotensin II fra |
| 26 | 35 | 100.0 | 7 | 17 | AAR95663 | Angiotensin II fra |
| 27 | 35 | 100.0 | 7 | 18 | AAW33318 | Targetting conjuga |
| 28 | 35 | 100.0 | 7 | 18 | AAW33010 | Targetting conjuga |
| 29 | 35 | 100.0 | 7 | 18 | AAW11202 | Targetting conjuga |
| 30 | 35 | 100.0 | 7 | 18 | AAW14976 | Conjugating peptid |
| 31 | 35 | 100.0 | 7 | 19 | AAW65598 | Angiotensin II ana |
| 32 | 35 | 100.0 | 7 | 19 | AAW65600 | Angiotensin II ana |
| 33 | 35 | 100.0 | 7 | 19 | AAW64729 | Angiotensin II pep |
| 34 | 35 | 100.0 | 7 | 19 | AAW64731 | Angiotensin II pep |
| 35 | 35 | 100.0 | 7 | 19 | AAW65633 | Angiotensin III an |
| 36 | 35 | 100.0 | 7 | 19 | AAW65641 | Angiotensin III an |
| 37 | 35 | 100.0 | 7 | 19 | AAW71111 | Peptide AII(2-8) u |
| 38 | 35 | 100.0 | 7 | 19 | AAW71113 | Peptide AII(1-7) u |
| 39 | 35 | 100.0 | 7 | 20 | AAY49587 | Angiotensin analog |
| 40 | 35 | 100.0 | 7 | 20 | AAY49589 | Angiotensin analog |
| 41 | 35 | 100.0 | 7 | 20 | AAY50296 | Neutrophil-activat |
| 42 | 35 | 100.0 | 7 | 20 | AAY50298 | Neutrophil-activat |
| 43 | 35 | 100.0 | 7 | 20 | AAY33902 | Angiotensin II ana |
| 44 | 35 | 100.0 | 7 | 20 | AAY33904 | Angiotensin II ana |
| 45 | 35 | 100.0 | 7 | 20 | AAY30540 | Amino acid sequenc |

ALIGNMENTS

RESULT 1
AAR95666
ID AAR95666 standard; peptide; 6 AA.
XX
AC AAR95666;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(2-7).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 2
AAW65601
ID AAW65601 standard; peptide; 6 AA.
XX
AC AAW65601;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(2-7).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 3
AAW64732
ID AAW64732 standard; peptide; 6 AA.
XX
AC AAW64732;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #4.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in

CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 4
AAW71114
ID AAW71114 standard; peptide; 6 AA.
XX
AC AAW71114;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(2-7) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 5
AAW65540
ID AAW65540 standard; peptide; 6 AA.
XX
AC AAW65540;
XX
DT 12-OCT-1998 (first entry)
XX
DE Peptide motif having affinity for angiotensin II receptor.
XX
KW Endothelin-1; angiotensin II receptor; imaging; cardiovascular disease;
KW losartan; contrast medium; diagnosis; lanthanide; biotin; lipopeptide;
KW fibrin-anti-polymerant peptide; motif.
XX
OS Synthetic.
XX
PN WO9818496-A2.
XX
PD 07-MAY-1998.
XX
PF 28-OCT-1997; 97WO-GB02956.
XX
PR 24-MAR-1997; 97GB-0006063.
PR 28-OCT-1996; 96GB-0022364.
PR 28-OCT-1996; 96GB-0022365.
PR 28-OCT-1996; 96GB-0022366.
PR 28-OCT-1996; 96GB-0022367.
PR 28-OCT-1996; 96GB-0022368.
PR 28-OCT-1996; 96GB-0022369.
PR 15-JAN-1997; 97GB-0000699.
PR 04-FEB-1997; 97GB-0002195.
XX
PA (COCK/) COCKBAIN J.
PA (NYCO-) NYCOMED IMAGING AS.
XX
PI Cuthbertson A, Klaveness J, Naevestad A;
XX
DR WPI; 1998-348067/30.
XX
PT New angiotensin II receptor binding compounds - useful for imaging
PT cardiovascular diseases and disorders
XX
PS Disclosure; Page 6; 99pp; English.
XX
CC The invention relates to organic compounds of formula V-L-R; V = organic
CC group having binding affinity for an angiotensin II receptor site; L = a
CC linker group or a bond; R = a group detectable in in vivo imaging of a
CC human or animal body; provided that when V is angiotensin or a peptidic
CC angiotensin derivative or analogue, then V-L-R is not a non-metal
CC radionuclide substituted peptide and L-V is not simply a peptide with a
CC chelating agent amide bonded to a side chain. Also claimed are: (1) 123I-
CC losartan and 131I-losartan; (2) the use of the organic compound for the
CC manufacture of a contrast medium for use in diagnosis involving
CC administration of the contrast medium to an animate subject and
CC generation of an image of at least part of the subject; (3) a method of
CC generating an image of an animate subject comprising administration of a
CC contrast agent comprising the organic compound and generating an image
CC of at least part of the subject and (4) a method of monitoring the
CC effect of treatment of animals with a drug to combat or provoke effects
CC associated with angiotensin II comprising administration of the organic

CC compound and detecting the uptake of the agent by angiotensin II
CC receptors, the administration and detection being optionally (and
CC preferably) effected repeatedly. The organic compounds are useful for
CC imaging cardiovascular diseases and disorders. The present sequence
CC is shown in the specification.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 6
AAY49590
ID AAY49590 standard; peptide; 6 AA.
XX
AC AAY49590;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:5.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 7
AAY33905
ID AAY33905 standard; peptide; 6 AA.
XX
AC AAY33905;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(2-7).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(2-7). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments, or AII
CC AT2 type 2 receptor agonists can rapidly provide a large population
CC of ESCs (Embryonic Stem Cell) for use in replacement therapy.
CC Similarly, methods that increase in vivo proliferation of ESCs will
CC enhance the utility of replacement therapy by rapidly increasing local
CC concentration of the stem cells and their progeny at the site of
CC therapy. The method also increases the potential utility of ESCs as
CC vehicles for gene therapy in certain disorders by more efficiently
CC providing a large number of such cells for transfection, and also by
CC providing a more efficient means to rapidly expand transfected ESCs.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6

```
          ||||||
Db      1 rvyihp 6


RESULT   8
AAY30543
ID   AAY30543 standard; peptide; 6 AA.
XX
AC   AAY30543;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII2-7.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents  -
XX
PS   Claim 2; Page 53; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   6 AA;


  Query Match             100.0%;  Score 35;  DB 20;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 rvyihp 6


RESULT   9
AAY30587
ID   AAY30587 standard; peptide; 6 AA.
XX
AC   AAY30587;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII2-7.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
KW   gene therapy; hematopoietic disorder.
XX
OS   Synthetic.
XX
PN   WO9945945-A1.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05194.
XX
PR   10-MAR-1998;   98US-0077382.
PR   09-APR-1998;   98US-0081262.
PR   30-APR-1998;   98US-0083670.
PR   19-JUN-1998;   98US-0090096.
PR   22-JUN-1998;   98US-0090216.
PR   11-SEP-1998;   98US-0099957.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA   (RODG/) RODGERS K E.
PA   (DIZE/) DIZEREGA G.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551209/46.
XX
PT   Use of angiotensin and angiotensin type peptides, for mitigating
PT   radiation induced tissue damage, improving bone marrow transplantation
PT   and promoting megakaryocyte and platelet production  -
XX
PS   Claim 2; Page 86; 116pp; English.
XX
CC   AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes a method for mitigating
CC   radiation induced tissue damage, improving the effectiveness of
CC   radiation therapy, to support bone marrow transplantation, and
CC   promoting megakaryocyte production and mobilization and platelet
CC   production. The method comprises administration of the present peptides.
CC   The methods can be used to mitigate radiation induced tissue damage, to
CC   improve the effectiveness of radiation therapy, to support bone marrow
CC   transplantation, and to promote megakaryocyte production and
CC   mobilization and platelet production. They are used particularly in
CC   cancer therapy. They can also be used to provide megakaryocytes as
CC   vehicles for gene therapy in hematopoietic disorders, by providing a
CC   more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ   Sequence   6 AA;


  Query Match             100.0%;  Score 35;  DB 20;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 rvyihp 6


RESULT  10
AAY32718
ID   AAY32718 standard; peptide; 6 AA.
XX
AC   AAY32718;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Angiotensin II analogue AII(2-7).
XX
KW   Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
```

KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 11
AAY33772
ID AAY33772 standard; peptide; 6 AA.
XX
AC AAY33772;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(2-7).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US03772.
XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 12
AAY15349
ID AAY15349 standard; peptide; 6 AA.
XX
AC AAY15349;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(2-7).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.

XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX
PS Claim 2; Page 9; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 13
AAY15309
ID AAY15309 standard; peptide; 6 AA.
XX
AC AAY15309;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(2-7).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a
CC decapeptide called angiotensin I (AI) which is converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY15339).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 1 rvyihp 6

RESULT 14
AAB27405
ID AAB27405 standard; Peptide; 6 AA.
XX
AC AAB27405;
XX
DT 23-JAN-2001 (first entry)
XX
DE Angiotensin II analog AII(2-7).
XX
KW Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW heart valve disease; myocarditis; angiotensin.
XX
OS Synthetic.
XX
PN WO200053211-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06198.
XX
PR 09-MAR-1999; 99US-0123678.
PR 31-AUG-1999; 99US-0151874.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers K, Dizerega G;
XX
DR WPI; 2000-611400/58.
XX
PT Promoting myocyte proliferation and myocardial tissue repair by
PT contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT for treating heart attacks, cardiomyopathies, inflammation and
PT infection -
XX
PS Claim 2; Page 10; 55pp; English.
XX
CC The present invention relates to a method of promoting myocyte
CC proliferation or differentiation by contacting myocytes with an active
CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and
CC angiotensin analogs. The present sequence is an angiotensin II analog
CC of the invention. The active agents of the invention may be useful for
CC promoting myocardial tissue repair following myocardial injury and for
CC treating heart failure in a mammal. Administration to accelerate in
CC vivo myocyte proliferation and/or to treat myocardial injuries can be
CC used to treat cardiomyopathies, inflammation, infection, sepsis,
CC ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC ischemia and infarction and for improving cardiac output by increasing
CC stroke volume.
XX
SQ Sequence 6 AA;

```
  Query Match             100.0%;  Score 35;  DB 21;  Length 6;
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Qy      1 RVYIHP 6
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Db      1 rvyihp 6


RESULT  15
AAB28103
ID   AAB28103 standard; Peptide; 6 AA.
XX
AC   AAB28103;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Angiotensin II analogue SEQ ID NO: 5.
XX
KW   Wound; scar formation; healing; adhesion formation; AII;
KW   angiotensin II analogue; scar treatment.
XX
OS   Synthetic.
XX
PN   WO200056345-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07669.
XX
PR   23-MAR-1999;   99US-0125707.
PR   16-JUN-1999;   99US-0139541.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-587607/55.
XX
PT   Limiting scar or adhesion formation comprises administering at least
PT   one active agent comprising a peptide -
XX
PS   Claim 2; Page 10; 54pp; English.
XX
CC   The present invention is concerned with peptide analogues of angiotensin
CC   II (AII) which can be used to limit scar and adhesion formation. The
CC   application of AII to wound tissue results in a rapid increase in the
CC   rate of wound healing and causes the proliferation of certain cells, such
CC   as epithelial cells and keratinocytes. Analogues of the protein have been
CC   shown to reduce scar formation, and can be used not only to limit new
CC   scar formation but also to therapeutically treat existing scars. The
CC   wound types include lacerations, burns, punctures, trauma, ulcers,
CC   periodontal conditions, laparotomy and incisional wounds, revision of
CC   hypertrophic scars, genetic hypertrophic scars, keloid scars,
CC   contractures after burns and cosmetic surgical procedures.
XX
SQ   Sequence   6 AA;


  Query Match             100.0%;  Score 35;  DB 21;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
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Db      1 rvyihp 6


Search completed: July  1, 2002, 07:41:55
Job time: 347 sec
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds
(without alignments)
2.480 Million cell updates/sec

Title: US-09-723-197-5
Perfect score: 35
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 35 | 100.0 | 6 | 2 | US-08-465-775-5 | Sequence 5, Appli |
| 2 | 35 | 100.0 | 6 | 3 | US-09-208-337-5 | Sequence 5, Appli |
| 3 | 35 | 100.0 | 6 | 3 | US-08-990-664-6 | Sequence 6, Appli |
| 4 | 35 | 100.0 | 6 | 4 | US-09-373-962-5 | Sequence 5, Appli |
| 5 | 35 | 100.0 | 6 | 4 | US-09-245-680-5 | Sequence 5, Appli |
| 6 | 35 | 100.0 | 6 | 4 | US-09-198-806C-5 | Sequence 5, Appli |
| 7 | 35 | 100.0 | 6 | 4 | US-09-352-191-5 | Sequence 5, Appli |
| 8 | 35 | 100.0 | 6 | 4 | US-09-012-400-5 | Sequence 5, Appli |
| 9 | 35 | 100.0 | 7 | 1 | US-08-021-839A-4 | Sequence 4, Appli |
| 10 | 35 | 100.0 | 7 | 1 | US-07-776-272-3 | Sequence 3, Appli |
| 11 | 35 | 100.0 | 7 | 1 | US-08-337-781-3 | Sequence 3, Appli |
| 12 | 35 | 100.0 | 7 | 2 | US-08-115-968-6 | Sequence 6, Appli |
| 13 | 35 | 100.0 | 7 | 2 | US-08-115-968-9 | Sequence 9, Appli |
| 14 | 35 | 100.0 | 7 | 2 | US-08-115-968-10 | Sequence 10, Appl |
| 15 | 35 | 100.0 | 7 | 2 | US-08-115-968-11 | Sequence 11, Appl |
| 16 | 35 | 100.0 | 7 | 2 | US-08-115-968-12 | Sequence 12, Appl |
| 17 | 35 | 100.0 | 7 | 2 | US-08-115-968-13 | Sequence 13, Appl |
| 18 | 35 | 100.0 | 7 | 2 | US-08-115-968-14 | Sequence 14, Appl |
| 19 | 35 | 100.0 | 7 | 2 | US-08-115-968-15 | Sequence 15, Appl |
| 20 | 35 | 100.0 | 7 | 2 | US-08-115-968-16 | Sequence 16, Appl |
| 21 | 35 | 100.0 | 7 | 2 | US-08-360-784B-3 | Sequence 3, Appli |
| 22 | 35 | 100.0 | 7 | 2 | US-08-465-775-2 | Sequence 2, Appli |
| 23 | 35 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 24 | 35 | 100.0 | 7 | 3 | US-09-054-308A-3 | Sequence 3, Appli |
| 25 | 35 | 100.0 | 7 | 3 | US-09-208-337-2 | Sequence 2, Appli |
| 26 | 35 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 27 | 35 | 100.0 | 7 | 3 | US-08-990-664-3 | Sequence 3, Appli |
| 28 | 35 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
| 29 | 35 | 100.0 | 7 | 3 | US-08-990-664-38 | Sequence 38, Appl |
| 30 | 35 | 100.0 | 7 | 3 | US-08-990-664-46 | Sequence 46, Appl |
| 31 | 35 | 100.0 | 7 | 4 | US-09-210-249-2 | Sequence 2, Appli |
| 32 | 35 | 100.0 | 7 | 4 | US-09-373-962-2 | Sequence 2, Appli |
| 33 | 35 | 100.0 | 7 | 4 | US-09-373-962-4 | Sequence 4, Appli |
| 34 | 35 | 100.0 | 7 | 4 | US-09-245-680-2 | Sequence 2, Appli |
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| 38 | 35 | 100.0 | 7 | 4 | US-09-352-191-2 | Sequence 2, Appli |
| 39 | 35 | 100.0 | 7 | 4 | US-09-352-191-4 | Sequence 4, Appli |
| 40 | 35 | 100.0 | 7 | 4 | US-09-012-400-2 | Sequence 2, Appli |
| 41 | 35 | 100.0 | 7 | 4 | US-09-012-400-4 | Sequence 4, Appli |
| 42 | 35 | 100.0 | 7 | 5 | PCT-US94-10258-6 | Sequence 6, Appli |
| 43 | 35 | 100.0 | 7 | 5 | PCT-US94-10258-9 | Sequence 9, Appli |
| 44 | 35 | 100.0 | 7 | 5 | PCT-US94-10258-10 | Sequence 10, Appl |
| 45 | 35 | 100.0 | 7 | 5 | PCT-US94-10258-11 | Sequence 11, Appl |

ALIGNMENTS

```
RESULT   1
US-08-465-775-5
; Sequence 5, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-5


  Query Match             100.0%;  Score 35;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
             ||||||
Db       1 RVYIHP 6
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RESULT   2
US-09-208-337-5
; Sequence 5, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-5


  Query Match             100.0%;  Score 35;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT   3
US-08-990-664-6
; Sequence 6, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-6


  Query Match             100.0%;  Score 35;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT   4
US-09-373-962-5
; Sequence 5, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (2-7)
US-09-373-962-5


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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
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Db      1 RVYIHP 6
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RESULT   5
US-09-245-680-5
; Sequence 5, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (2-7)
US-09-245-680-5


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
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Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT   6
US-09-198-806C-5
; Sequence 5, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (2-7)
US-09-198-806C-5


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT   7
US-09-352-191-5
; Sequence 5, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (2-7)
US-09-352-191-5


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
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Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT   8
US-09-012-400-5
; Sequence 5, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (2-7)
US-09-012-400-5


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Qy      1 RVYIHP 6
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Db      1 RVYIHP 6


RESULT   9
US-08-021-839A-4
; Sequence 4, Application US/08021839A
; Patent No. 5326776
;  GENERAL INFORMATION:
;    APPLICANT:  Winn, Martin
;    APPLICANT:  De, Biswanath
;    APPLICANT:  Zydowsky, Thomas M.
;    APPLICANT:  Kerkman, Daniel J.
;    APPLICANT:  DeBernardis, John F.
;    APPLICANT:  Rosenberg, Saul H.
;    APPLICANT:  Shiosaki, Kazumi
;    APPLICANT:  Basha, Fatima Z.
;    APPLICANT:  Spina, Kenneth P.
;    APPLICANT:  Von Geldern, Thomas W.
;    TITLE OF INVENTION:  Angiotensin II Receptor Antagonists
;    NUMBER OF SEQUENCES:  4
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edward H. Gorman, Jr.
;      STREET:  Abbott Laboratories
;      STREET:  D-377/AP6D
;      STREET:  One Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,800 Kb
;      COMPUTER:  Apple Macintosh IIci
;      OPERATING SYSTEM:  Macintosh
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/021,839A
;      FILING DATE:  24-FEB-1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/844,817
;      FILING DATE:  02-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steven R. Crowley
;      REGISTRATION NUMBER:  31,604
;      REFERENCE/DOCKET NUMBER:  5136.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708) 938-7742
;      TELEFAX:  (708) 938-2623
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acid residues
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:
;      DESCRIPTION:  peptide
US-08-021-839A-4


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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
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Db      1 RVYIHP 6


RESULT  10
US-07-776-272-3
; Sequence 3, Application US/07776272
; Patent No. 5612454
;  GENERAL INFORMATION:
;    APPLICANT:  Kaminuma, Toshihiko
;    APPLICANT:  Iida, Toshii
;    APPLICANT:  Tajima, Masahiro
;    TITLE OF INVENTION:  Process for Purification of Polypeptide
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wegner, Cantor, Mueller & Player
;      STREET:  1233 20th St. N.W.  P.O. Box 18218
;      CITY:  Washington
;      STATE:  District of Columbia
;      COUNTRY:  United States of America
;      ZIP:  20036-8218
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/776,272
;      FILING DATE:  19911129
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  P-450-23167
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-0400
;      TELEFAX:  202-887-0605
;      TELEX:  440706
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
US-07-776-272-3


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT  11
US-08-337-781-3
; Sequence 3, Application US/08337781
; Patent No. 5629292
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN III AND ANALOGS
;    TITLE OF INVENTION:  THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 No. 5629292th Figueroa Street, Fifth Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/337,781
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-336C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-337-781-3


  Query Match           100.0%;  Score 35;  DB 1;  Length 7;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RVYIHP 6
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Db      1 RVYIHP 6


RESULT 12
US-08-115-968-6
; Sequence 6, Application US/08115968
; Patent No. 5824696
;  GENERAL INFORMATION:
;    APPLICANT:  Griswold E, Don
;    APPLICANT:  Wharton, John
;    TITLE OF INVENTION:  Medicaments
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham
;      STREET:  P. O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/115,968
;      FILING DATE:  01-SEP-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dinner, Dara L
;      REGISTRATION NUMBER:  33,680
;      REFERENCE/DOCKET NUMBER:  P50192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 270-5017
;      TELEFAX:  (610) 270-5090
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Inhibitory-site
;      LOCATION:  1..2
;      OTHER INFORMATION:  /product= "other"
;      OTHER INFORMATION:  /note= "hydroxyacetal of Arg"
;    FEATURE:
;      NAME/KEY:  Inhibitory-site
;      LOCATION:  6..7
;      OTHER INFORMATION:  /product= "other"
;      OTHER INFORMATION:  /note= "methyl ester of Thr"
US-08-115-968-6


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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
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Db      1 RVYIHP 6


RESULT 13
US-08-115-968-9
; Sequence 9, Application US/08115968
; Patent No. 5824696
;  GENERAL INFORMATION:
;    APPLICANT:  Griswold E, Don
;    APPLICANT:  Wharton, John
;    TITLE OF INVENTION:  Medicaments
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham
;      STREET:  P. O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/115,968
;      FILING DATE:  01-SEP-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dinner, Dara L
;      REGISTRATION NUMBER:  33,680
;      REFERENCE/DOCKET NUMBER:  P50192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 270-5017
;      TELEFAX:  (610) 270-5090
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Inhibitory-site
;      LOCATION:  1..2
;      OTHER INFORMATION:  /product= "other"
;      OTHER INFORMATION:  /note= "aminoocyacetyl deriv of arg"
US-08-115-968-9


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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT 14
US-08-115-968-10
; Sequence 10, Application US/08115968
; Patent No. 5824696
;  GENERAL INFORMATION:
;    APPLICANT:  Griswold E, Don
;    APPLICANT:  Wharton, John
;    TITLE OF INVENTION:  Medicaments
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham
;      STREET:  P. O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/115,968
;      FILING DATE:  01-SEP-1993
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;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dinner, Dara L
;      REGISTRATION NUMBER:  33,680
;      REFERENCE/DOCKET NUMBER:  P50192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 270-5017
;      TELEFAX:  (610) 270-5090
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Inhibitory-site
;      LOCATION:  1..2
;      OTHER INFORMATION:  /product= "other"
;      OTHER INFORMATION:  /note= "aminooxypropionyl deriv of arg"
US-08-115-968-10


  Query Match             100.0%;  Score 35;  DB 2;  Length 7;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db      1 RVYIHP 6


RESULT  15
US-08-115-968-11
; Sequence 11, Application US/08115968
; Patent No. 5824696
;  GENERAL INFORMATION:
;    APPLICANT:  Griswold E, Don
;    APPLICANT:  Wharton, John
;    TITLE OF INVENTION:  Medicaments
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham
;      STREET:  P. O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/115,968
;      FILING DATE:  01-SEP-1993
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dinner, Dara L
;      REGISTRATION NUMBER:  33,680
;      REFERENCE/DOCKET NUMBER:  P50192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 270-5017
;      TELEFAX:  (610) 270-5090
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Inhibitory-site
;      LOCATION:  1..2
;      OTHER INFORMATION:  /product= "other"
;      OTHER INFORMATION:  /note= "hydroxyacetal deriv of arg"
US-08-115-968-11


  Query Match             100.0%;  Score 35;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
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Db      1 RVYIHP 6


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:27 ; Search time 69.93 Seconds
(without alignments)
8.244 Million cell updates/sec

Title: US-09-723-197-5
Perfect score: 35
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 35 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 3 | 35 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 4 | 35 | 100.0 | 476 | 1 | JC2318 | angiotensin precur |
| 5 | 35 | 100.0 | 477 | 1 | ANRT | angiotensin precur |
| 6 | 35 | 100.0 | 477 | 1 | A29978 | angiotensin precur |
| 7 | 35 | 100.0 | 485 | 1 | ANHU | angiotensin precur |
| 8 | 35 | 100.0 | 540 | 2 | S72233 | transcription fact |
| 9 | 34 | 97.1 | 10 | 2 | A60624 | angiotensin I - Ja |
| 10 | 34 | 97.1 | 10 | 2 | A90917 | angiotensin precur |
| 11 | 34 | 97.1 | 10 | 2 | A90345 | angiotensin precur |
| 12 | 34 | 97.1 | 316 | 2 | T34838 | probable transfera |
| 13 | 33 | 94.3 | 11 | 2 | S07207 | Crinia-angiotensin |
| 14 | 32 | 91.4 | 177 | 2 | C71329 | hypothetical prote |
| 15 | 32 | 91.4 | 444 | 2 | T20803 | hypothetical prote |
| 16 | 32 | 91.4 | 681 | 2 | I78558 | hypothetical Brach |
| 17 | 32 | 91.4 | 695 | 2 | T24950 | hypothetical prote |
| 18 | 32 | 91.4 | 701 | 1 | S46458 | transcription fact |
| 19 | 32 | 91.4 | 702 | 2 | G01840 | T-box protein 2 - |
| 20 | 32 | 91.4 | 974 | 1 | A40213 | optic lobe develop |
| 21 | 31 | 88.6 | 173 | 2 | S72230 | transcription fact |
| 22 | 31 | 88.6 | 184 | 2 | S72231 | transcription fact |
| 23 | 31 | 88.6 | 274 | 2 | B90430 | hypothetical prote |
| 24 | 31 | 88.6 | 288 | 2 | T48753 | conserved hypothet |
| 25 | 31 | 88.6 | 300 | 2 | S24057 | ferritin 2 precurs |
| 26 | 31 | 88.6 | 370 | 2 | AC0173 | probable iron-sulf |
| 27 | 31 | 88.6 | 482 | 1 | VHVUCH | nucleocapsid prote |
| 28 | 31 | 88.6 | 485 | 1 | VHVUHJ | nucleoprotein - Ha |
| 29 | 31 | 88.6 | 539 | 2 | T46720 | hypothetical prote |
| 30 | 31 | 88.6 | 611 | 2 | F70325 | conserved hypothet |
| 31 | 31 | 88.6 | 617 | 2 | S10511 | thrombin (EC 3.4.2 |
| 32 | 31 | 88.6 | 622 | 1 | TBHU | thrombin (EC 3.4.2 |
| 33 | 31 | 88.6 | 625 | 1 | TBBO | thrombin (EC 3.4.2 |
| 34 | 31 | 88.6 | 646 | 2 | T38171 | probable serine/th |
| 35 | 30 | 85.7 | 169 | 2 | D64443 | mutator protein mu |
| 36 | 30 | 85.7 | 184 | 2 | AC1584 | hypothetical prote |
| 37 | 30 | 85.7 | 228 | 2 | E75469 | conserved hypothet |
| 38 | 30 | 85.7 | 277 | 2 | E86229 | hypothetical prote |
| 39 | 30 | 85.7 | 289 | 2 | C96610 | hypothetical prote |
| 40 | 30 | 85.7 | 349 | 2 | T50372 | probable ATP-depen |
| 41 | 30 | 85.7 | 385 | 2 | G84459 | probable GDP-manno |
| 42 | 30 | 85.7 | 387 | 2 | JC5556 | adhalin - mouse |
| 43 | 30 | 85.7 | 387 | 2 | I48201 | adhalin - golden h |
| 44 | 30 | 85.7 | 415 | 2 | G96778 | hypothetical prote |
| 45 | 30 | 85.7 | 423 | 1 | A49125 | gastrulation regul |

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 35; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 2 RVYIHP 7

RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 35; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 2 RVYIHP 7

RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 35; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 2 RVYIHP 7

RESULT 4
JC2318
angiotensin precursor - sheep
N;Alternate names: angiotensinogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC2318; A25406
R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
A;Reference number: JC2318; MUID:95072318
A;Accession: JC2318
A;Molecule type: mRNA
A;Residues: 1-476 <NAG>
A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 465 as Leu
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A;Title: Purification and characterization of ovine angiotensinogen.
A;Reference number: A25406; MUID:86136099
A;Accession: A25406
A;Molecule type: protein
A;Residues: 25-37,'X',39 <FER>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-476/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin #status predicted <MAT>
F;295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 26 RVYIHP 31

RESULT 5
ANRT

angiotensin precursor - rat
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849
A;Accession: A93945
A;Molecule type: mRNA
A;Residues: 1-477 <OHK>
A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, char
A;Reference number: A90456; MUID:82091819
A;Accession: A90456
A;Molecule type: protein
A;Residues: 25-41 <BOU>
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin I #status experimental <PP1>
F;25-32/Product: angiotensin II #status experimental <PP2>
F;26-32/Product: angiotensin III #status experimental <PP3>
F;295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
||||||
Db 26 RVYIHP 31

RESULT 6
A29978
angiotensin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29978
R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A;Title: Molecular cloning of the mouse angiotensinogen gene.
A;Reference number: A29978; MUID:88284703
A;Accession: A29978
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-477 <CLO>
A;Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427
C;Genetics:
A;Introns: 277/1; 366/2; 414/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MAT>

Query Match 100.0%; Score 35; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6

```
          ||||||
Db      26 RVYIHP 31


RESULT   7
ANHU
angiotensin precursor [validated] - human
N;Alternate names: angiotensinogen
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1982 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: A35203; A31362; I37168; I37169; A60825; I39462; A90487; A90226; I54281; A01
R;Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,
J. Biol. Chem. 265, 7576-7582, 1990
A;Title: Structure and expression of the human angiotensinogen gene. Identification of a
A;Reference number: A35203; MUID:90237063
A;Accession: A35203
A;Molecule type: DNA
A;Residues: 1-485 <FUK>
A;Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
R;Gaillard, I.; Clauser, E.; Corvol, P.
DNA 8, 87-99, 1989
A;Title: Structure of human angiotensinogen gene.
A;Reference number: A31362; MUID:89170129
A;Accession: A31362
A;Molecule type: DNA
A;Residues: 1-267,'M',269-332,'E',334-485 <GAI>
A;Cross-references: GB:M24686; GB:M24687; GB:M24688
A;Note: the authors translated the codon GAA for residue 333 as Gln
R;Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.
J. Biol. Chem. 269, 28598-28605, 1994
A;Title: Identification of cell type-dependent enhancer core element located in the 3'-d
A;Reference number: I37168; MUID:95050659
A;Accession: I37168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <NIB1>
A;Cross-references: EMBL:X15324; NID:g1197496; PIDN:CAA33385.1; PID:g1197497
A;Accession: I37169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 287-375 <NIB2>
A;Cross-references: EMBL:X15325; NID:g28695
R;Kunapuli, S.P.; Benedict, C.R.; Kumar, A.
Arch. Biochem. Biophys. 254, 642-646, 1987
A;Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.
A;Reference number: A60825; MUID:87212053
A;Accession: A60825
A;Molecule type: mRNA
A;Residues: 32-184 <KUN1>
R;Kunapuli, S.P.; Kumar, A.
Circ. Res. 60, 786-790, 1987
A;Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence o
A;Reference number: I39462; MUID:87244745
A;Accession: I39462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-338 <KUN2>
A;Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181
R;Kageyama, R.; Ohkubo, H.; Nakanishi, S.
Biochemistry 23, 3603-3609, 1984
A;Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ
A;Reference number: A90487; MUID:85000455
A;Accession: A90487
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-485 <KAG>
A;Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640
A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
R;Tewksbury, D.A.; Dart, R.A.; Travis, J.
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
A;Title: The amino terminal amino acid sequence of human angiotensinogen.
A;Reference number: A90226; MUID:81255848
A;Accession: A90226
A;Molecule type: protein
A;Residues: 34-46,'X',48-50,'S',52-57,'D' <TEW>
R;Hixson, J.E.; Powers, P.K.
Hum. Genet. 96, 110-112, 1995
A;Title: Detection and characterization of new mutations in the human angiotensinogen
A;Reference number: I54281; MUID:95331754
A;Accession: I54281
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 176-241,'I',243-267,'M',269-287,'ANLSAG' <HIX>
A;Cross-references: GB:S78529; NID:g999316; PIDN:AAD14287.1; PID:g4261987
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,
o induces thirst.
C;Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
C;Genetics:
A;Gene: GDB:AGT
A;Cross-references: GDB:118750; OMIM:106150
A;Map position: 1q42-1q43
A;Introns: 286/1; 375/2; 423/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>
F;34-485/Product: angiotensinogen #status predicted <MPT>
F;34-43/Product: angiotensin I #status experimental <PP1>
F;34-41/Product: angiotensin II #status experimental <PP2>
F;35-41/Product: angiotensin III #status experimental <PP3>
F;47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 35;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           ||||||
Db      35 RVYIHP 40


RESULT   8
S72233
transcription factor tbx6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S72233; S72232
R;Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.
submitted to the EMBL Data Library, May 1996
A;Reference number: S72233
A;Accession: S72233
A;Molecule type: mRNA
A;Residues: 1-540 <AGU>
A;Cross-references: EMBL:U57331; NID:g1620601; PIDN:AAC53110.1; PID:g1620602
R;Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B
Genetics 144, 249-254, 1996
A;Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.
A;Reference number: S72230; MUID:97032942
A;Accession: S72232
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 100-280 <AGW>
A;Cross-references: EMBL:U57331
C;Genetics:
A;Gene: tbx6
C;Superfamily: T-box homology
C;Keywords: DNA binding
F;100-282/Domain: T-box homology <TBX>


  Query Match             100.0%;  Score 35;  DB 2;  Length 540;
```

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          ||||||
Db    171 RVYIHP 176
```

RESULT 9
A60624
angiotensin I - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of thes
A;Reference number: A60624; MUID:90284684
A;Accession: A60624
A;Molecule type: protein
A;Residues: 1-10 <TAK>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.1%; Score 34; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7
```

RESULT 10
A90917
angiotensin precursor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90917; A01250
R;Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A;Reference number: A90917; MUID:74127845
A;Accession: A90917
A;Molecule type: protein
A;Residues: 1-10 <NAK>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 34; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7
```

RESULT 11
A90345
angiotensin precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90345; A01250
R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 34; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7
```

RESULT 12
T34838
probable transferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34838
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21559
A;Accession: T34838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-316 <OLI>
A;Cross-references: EMBL:AL035478; PIDN:CAB36592.1; GSPDB:GN00070; SCOEDB:SC2G5.05
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC2G5.05

Query Match 97.1%; Score 34; DB 2; Length 316;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          |||:||
Db    218 RVYVHP 223
```

RESULT 13
S07207
Crinia-angiotensin, skin - frog (Crinia georgiana)
C;Species: Crinia georgiana
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C;Accession: S07207
R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A;Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II
A;Reference number: S07207; MUID:80024575
A;Accession: S07207
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides

Query Match 94.3%; Score 33; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 0.48;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RVYIHP 6
          |:|:||
Db      5 RIYVHP 10
```

RESULT 14
C71329
hypothetical protein TP0404 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C;Accession: C71329
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: C71329
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-177 <COL>
A;Cross-references: GB:AE001218; GB:AE000520; NID:g3322678; PIDN:AAC65395.1; PID:g332269
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0404

Query Match 91.4%; Score 32; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
:|||||
Db 2 KVYIHP 7

RESULT 15
T20803
hypothetical protein F12F6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20803
R;Kershaw, J.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19326
A;Accession: T20803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z73425; PIDN:CAA97789.1; GSPDB:GN00022; CESP:F12F6.3
A;Experimental source: clone F12F6
C;Genetics:
A;Gene: CESP:F12F6.3
A;Map position: 4
A;Introns: 27/2; 75/2; 101/2; 161/3; 188/3; 243/3; 284/2; 388/3; 428/3

Query Match 91.4%; Score 32; DB 2; Length 444;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6
:|||||
Db 46 KVYIHP 51

Search completed: July 1, 2002, 07:46:28
Job time: 449 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:07 ; Search time 34.05 Seconds
(without alignments)
6.823 Million cell updates/sec

Title: US-09-723-197-5
Perfect score: 35
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 35 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 35 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 3 | 35 | 100.0 | 436 | 1 | TBX6_HUMAN | O95947 homo sapien |
| 4 | 35 | 100.0 | 476 | 1 | ANGT_SHEEP | P20757 ovis aries |
| 5 | 35 | 100.0 | 477 | 1 | ANGT_MOUSE | P11859 mus musculu |
| 6 | 35 | 100.0 | 477 | 1 | ANGT_RAT | P01015 rattus norv |
| 7 | 35 | 100.0 | 485 | 1 | ANGT_HUMAN | P01019 homo sapien |
| 8 | 35 | 100.0 | 501 | 1 | TX18_HUMAN | O95935 homo sapien |
| 9 | 35 | 100.0 | 540 | 1 | TBX6_MOUSE | P70327 mus musculu |
| 10 | 35 | 100.0 | 602 | 1 | TX15_MOUSE | O70306 mus musculu |
| 11 | 35 | 100.0 | 613 | 1 | TX18_MOUSE | Q9epz6 mus musculu |
| 12 | 34 | 97.1 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 13 | 34 | 97.1 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 14 | 34 | 97.1 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 15 | 33 | 94.3 | 11 | 1 | ANGT_CRIGE | P09037 crinia geor |
| 16 | 32 | 91.4 | 177 | 1 | Y404_TREPA | O83419 treponema p |
| 17 | 32 | 91.4 | 378 | 1 | EXT1_CAEEL | O01704 caenorhabdi |
| 18 | 32 | 91.4 | 414 | 1 | TBX3_CHICK | O73718 gallus gall |
| 19 | 32 | 91.4 | 681 | 1 | TBR1_MOUSE | Q64336 mus musculu |
| 20 | 32 | 91.4 | 682 | 1 | TBR1_HUMAN | Q16650 homo sapien |
| 21 | 32 | 91.4 | 701 | 1 | TBX2_MOUSE | Q60707 mus musculu |
| 22 | 32 | 91.4 | 702 | 1 | TBX2_HUMAN | Q13207 homo sapien |
| 23 | 32 | 91.4 | 742 | 1 | TBX3_HUMAN | O15119 homo sapien |
| 24 | 32 | 91.4 | 988 | 1 | OMB_DROME | Q24432 drosophila |
| 25 | 31 | 88.6 | 173 | 1 | TBX4_MOUSE | P70325 mus musculu |
| 26 | 31 | 88.6 | 251 | 1 | TX20_HUMAN | Q9umr3 homo sapien |
| 27 | 31 | 88.6 | 297 | 1 | TX20_MOUSE | Q9es03 mus musculu |
| 28 | 31 | 88.6 | 300 | 1 | FRI2_MAIZE | P29390 zea mays (m |
| 29 | 31 | 88.6 | 482 | 1 | NCAP_CCHFV | P27317 crimean-con |
| 30 | 31 | 88.6 | 485 | 1 | NCAP_HAZVJ | P27318 hazara viru |
| 31 | 31 | 88.6 | 518 | 1 | TBX5_HUMAN | Q99593 homo sapien |
| 32 | 31 | 88.6 | 518 | 1 | TBX5_MOUSE | P70326 mus musculu |
| 33 | 31 | 88.6 | 535 | 1 | TX21_HUMAN | Q9ul17 homo sapien |
| 34 | 31 | 88.6 | 545 | 1 | TBX4_HUMAN | P57082 homo sapien |
| 35 | 31 | 88.6 | 617 | 1 | THRB_RAT | P18292 rattus norv |
| 36 | 31 | 88.6 | 622 | 1 | THRB_HUMAN | P00734 homo sapien |
| 37 | 31 | 88.6 | 625 | 1 | THRB_BOVIN | P00735 bos taurus |
| 38 | 31 | 88.6 | 646 | 1 | KDBE_SCHPO | Q10364 schizosacch |
| 39 | 31 | 88.6 | 692 | 1 | EOMD_XENLA | P79944 xenopus lae |
| 40 | 31 | 88.6 | 981 | 1 | EPA3_BRARE | O13146 brachydanio |
| 41 | 30 | 85.7 | 169 | 1 | ADPP_METJA | Q58549 methanococc |
| 42 | 30 | 85.7 | 361 | 1 | TBXL_CHICK | P79779 gallus gall |
| 43 | 30 | 85.7 | 387 | 1 | SGCA_MESAU | Q64255 mesocricetu |
| 44 | 30 | 85.7 | 387 | 1 | SGCA_MOUSE | P82350 mus musculu |
| 45 | 30 | 85.7 | 397 | 1 | TBXT_CHICK | P79778 gallus gall |

ALIGNMENTS

```
RESULT   1
ANG2_BOTJA
ID   ANG2_BOTJA     STANDARD;      PRT;     8 AA.
AC   Q10582;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Angiotensin-like peptide II (Fragment).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=96208932; PubMed=8829801;
RA   Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  1046 MW;  DDD761E04B42D40A CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           ||||||
Db       2 RVYIHP 7


RESULT   2
ANGT_HORSE
ID   ANGT_HORSE     STANDARD;      PRT;    14 AA.
AC   P01016;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE.
RA   Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT   "The preparation, purification, and amino acid sequence of a
RT   polypeptide renin substrate.";
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RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
            ||||||
Db      2 RVYIHP 7


RESULT   3
TBX6_HUMAN
ID   TBX6_HUMAN     STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
RN   [2]
RP   SEQUENCE OF 135-272 FROM N.A.
RC   TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 4.8;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
            ||||||
Db    171 RVYIHP 176


RESULT   4
ANGT_SHEEP
ID   ANGT_SHEEP     STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    476       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     26 RVYIHP 31


RESULT   5
ANGT_MOUSE
ID   ANGT_MOUSE     STANDARD;      PRT;   477 AA.
AC   P11859;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88284703; PubMed=3397061;
RA   Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT   "Molecular cloning of the mouse angiotensinogen gene.";
RL   Genomics 2:240-248(1988).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF045887; AAC01765.1; -.
DR   EMBL; AF045886; AAC01765.1; JOINED.
DR   EMBL; AF045885; AAC01765.1; JOINED.
DR   EMBL; AF045884; AAC01765.1; JOINED.
DR   PIR; A29978; A29978.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51990 MW;  A877F4029F338607 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     26 RVYIHP 31


RESULT   6
ANGT_RAT
ID   ANGT_RAT       STANDARD;      PRT;   477 AA.
AC   P01015;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR;
RX   MEDLINE=83169849; PubMed=6572971;
RA   Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA   Nakanishi S.;
RT   "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN   [2]
RP   SEQUENCE OF 25-34.
RX   MEDLINE=73060322; PubMed=4344907;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. II. Structure of rat
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 20:1579-1581(1972).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L00094; AAA98779.1; -.
DR   EMBL; L00091; AAA98779.1; JOINED.
DR   EMBL; L00092; AAA98779.1; JOINED.
DR   EMBL; L00093; AAA98779.1; JOINED.
DR   PIR; A01251; ANRT.
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DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL       1    24
FT   CHAIN       25   477       ANGIOTENSINOGEN.
FT   PEPTIDE     25    34       ANGIOTENSIN I.
FT   PEPTIDE     25    32       ANGIOTENSIN II.
FT   CARBOHYD   295   295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   319   319       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51981 MW;  689051A5788D693D CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     26 RVYIHP 31


RESULT   7
ANGT_HUMAN
ID   ANGT_HUMAN     STANDARD;      PRT;   485 AA.
AC   P01019; Q16358; Q16359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89170129; PubMed=2924688;
RA   Gaillard I., Clauser E., Corvol P.;
RT   "Structure of human angiotensinogen gene.";
RL   DNA 8:87-99(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85000455; PubMed=6089875;
RA   Kageyama R., Ohkubo H., Nakanishi S.;
RT   "Primary structure of human preangiotensinogen deduced from the
RT   cloned cDNA sequence.";
RL   Biochemistry 23:3603-3609(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90237063; PubMed=1692023;
RA   Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA   Murakami K.;
RT   "Structure and expression of the human angiotensinogen gene.
RT   Identification of a unique and highly active promoter.";
RL   J. Biol. Chem. 265:7576-7582(1990).
RN   [4]
RP   SEQUENCE OF 1-338 FROM N.A.
RX   MEDLINE=87244745; PubMed=2885106;
RA   Kunapuli S.P., Kumar A.;
RT   "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT   presence of its mRNA in rat heart.";
RL   Circ. Res. 60:786-790(1987).
RN   [5]
RP   SEQUENCE OF 34-45, AND SUBUNITS.
RC   TISSUE=Serum;
RX   MEDLINE=95293954; PubMed=7539791;
RA   Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA   Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT   "Identification of angiotensinogen and complement C3dg as novel
RT   proteins binding the proform of eosinophil major basic protein in
RT   human pregnancy serum and plasma.";
RL   J. Biol. Chem. 270:13645-13651(1995).
RN   [6]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=69014170; PubMed=4300938;
RA   Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT   "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL   Biochim. Biophys. Acta 168:106-112(1968).
RN   [7]
RP   STRUCTURE BY NMR OF ANGIOTENSIN II.
RX   MEDLINE=98151281; PubMed=9492317;
RA   Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT   "The octapeptide angiotensin II adopts a well-defined structure in a
RT   phospholipid environment.";
RL   Eur. J. Biochem. 251:448-453(1998).
RN   [8]
RP   VARIANTS MET-207; THR-268 AND CYS-281.
RX   MEDLINE=93008239; PubMed=1394429;
RA   Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA   Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA   Lalouel J.-M., Corvol P.;
RT   "Molecular basis of human hypertension: role of angiotensinogen.";
RL   Cell 71:169-180(1992).
RN   [9]
RP   VARIANT THR-268.
RX   MEDLINE=93291876; PubMed=8513325;
RA   Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA   Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
RA   Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT   "A molecular variant of angiotensinogen associated with
RT   preeclampsia.";
RL   Nat. Genet. 4:59-61(1993).
RN   [10]
RP   VARIANTS ILE-242; ARG-244 AND CYS-281.
RX   MEDLINE=95331754; PubMed=7607642;
RA   Hixson J.E., Powers P.K.;
RT   "Detection and characterization of new mutations in the human
RT   angiotensinogen gene (AGT).";
RL   Hum. Genet. 96:110-112(1995).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
CC       heterotetramer with the proform of PRG2 and as a complex (probably
CC       a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
CC       ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
CC       (PIH) (PREECLAMPSIA).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02215; AAA51731.1; -.
DR   EMBL; M24689; AAA51679.1; -.
DR   EMBL; M24686; AAA51679.1; JOINED.
DR   EMBL; M24687; AAA51679.1; JOINED.
DR   EMBL; M24688; AAA51679.1; JOINED.
DR   EMBL; X15324; CAA33385.1; -.
DR   EMBL; X15325; CAA33385.1; JOINED.
DR   EMBL; X15326; CAA33385.1; JOINED.
DR   EMBL; X15327; CAA33385.1; JOINED.
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DR   EMBL; M69110; AAA52282.1; -.
DR   EMBL; S78529; AAD14287.1; -.
DR   EMBL; S78530; AAD14288.1; -.
DR   PIR; A01249; ANHU.
DR   PIR; A31362; A31362.
DR   PIR; A35203; A35203.
DR   SWISS-2DPAGE; P01019; HUMAN.
DR   MIM; 106150; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW   Disease mutation; Polymorphism.
FT   SIGNAL       1     33
FT   CHAIN       34    485       ANGIOTENSINOGEN.
FT   PEPTIDE     34     43       ANGIOTENSIN I.
FT   PEPTIDE     34     41       ANGIOTENSIN II.
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    207    207       T -> M.
FT                               /FTId=VAR_007093.
FT   VARIANT    242    242       T -> I (IN HYPERTENSION).
FT                               /FTId=VAR_007094.
FT   VARIANT    244    244       L -> R (IN HYPERTENSION).
FT                               /FTId=VAR_007095.
FT   VARIANT    268    268       M -> T (IN HYPERTENSION).
FT                               /FTId=VAR_007096.
FT   VARIANT    281    281       Y -> C (IN HYPERTENSION).
FT                               /FTId=VAR_007097.
FT   CONFLICT   333    333       Q -> E (IN REF. 1).
SQ   SEQUENCE   485 AA;  53154 MW;  5026C2DFB2DD236E CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 5.4;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT   8
TX18_HUMAN
ID   TX18_HUMAN     STANDARD;      PRT;   501 AA.
AC   O95935; Q9UJI6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX18 (T-box protein 18) (Fragment).
GN   TBX18.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bates K.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 42-223 FROM N.A.
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AL035694; CAB45196.1; -.
DR   EMBL; AJ010278; CAB37937.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 604613; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   NON_TER      1      1
FT   DNA_BIND    42    224       T-BOX.
SQ   SEQUENCE   501 AA;  54229 MW;  45A732B009A4E5F5 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db    115 RVYIHP 120


RESULT   9
TBX6_MOUSE
ID   TBX6_MOUSE     STANDARD;      PRT;   540 AA.
AC   P70327;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97032942; PubMed=8878690;
RA   Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA   Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT   "Evolution of mouse T-box genes by tandem duplication and cluster
RT   dispersion.";
RL   Genetics 144:249-254(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastrula;
RX   MEDLINE=97115702; PubMed=8954725;
RA   Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT   "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT   gastrulation.";
RL   Dev. Biol. 180:534-542(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=98140705; PubMed=9490412;
RA   Chapman D.L., Papaioannou V.E.;
RT   "Three neural tubes in mouse embryos with mutations in the T-box gene
```

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RT   Tbx6.";
RL   Nature 391:695-697(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC       MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC       DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC       PATHWAY.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC       STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC       MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC       PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC       AS THE SOURCE OF MESODERM.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U57331; AAC53110.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:102539; Tbx6.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       61     64       POLY-ALA.
FT   DOMAIN       79     82       POLY-PRO.
FT   DNA_BIND    100    273       T-BOX.
SQ   SEQUENCE   540 AA;  58628 MW;  BC834CE2745E8E61 CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db    171 RVYIHP 176


RESULT  10
TX15_MOUSE
ID   TX15_MOUSE     STANDARD;      PRT;   602 AA.
AC   O70306; O54840;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX15 (T-box protein 15) (MmTBx8).
GN   TBX15 OR TBX14 OR TBX8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98360093; PubMed=9693034;
RA   Agulnik S.I., Papaioannou V.E., Silver L.M.;
RT   "Cloning, mapping, and expression analysis of TBX15, a new member of
RT   the T-Box gene family.";
RL   Genomics 51:68-75(1998).
RN   [2]
RP   SEQUENCE OF 44-602 FROM N.A.
RX   MEDLINE=98163742; PubMed=9503012;
RA   Wattler S., Russ A., Evans M., Nehls M.;
RT   "A combined analysis of genomic and primary protein structure defines
RT   the phylogenetic relationship of new members if the T-box family.";
RL   Genomics 48:24-33(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF041822; AAC32316.1; -.
DR   EMBL; AF013282; AAC40115.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:1277234; Tbx15.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DNA_BIND    122    304       T-BOX.
FT   CONFLICT    100    102       RAT -> AGP (IN REF. 2).
FT   CONFLICT    309    309       G -> R (IN REF. 2).
SQ   SEQUENCE   602 AA;  65805 MW;  BC59DA8E6B09F72B CRC64;


  Query Match             100.0%;  Score 35;  DB 1;  Length 602;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db    195 RVYIHP 200


RESULT  11
TX18_MOUSE
ID   TX18_MOUSE     STANDARD;      PRT;   613 AA.
AC   Q9EPZ6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX18 (T-box protein 18).
GN   TBX18.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   PubMed=11118889;
RA   Kraus F., Haenig B., Kispert A.;
RT   "Cloning and expression analysis of the mouse T-box gene Tbx18.";
RL   Mech. Dev. 100:83-86(2001).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF306666; AAG48598.1; -.
DR   MGD; MGI:1923615; Tbx18.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DNA_BIND    149    336       T-BOX.
SQ   SEQUENCE   613 AA;  65463 MW;  A9E64D395725AB38 CRC64;


  Query Match            100.0%;  Score 35;  DB 1;  Length 613;
  Best Local Similarity  100.0%;  Pred. No. 6.8;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db    227 RVYIHP 232


RESULT  12
ANG1_BOTJA
ID   ANG1_BOTJA     STANDARD;      PRT;    10 AA.
AC   Q10581;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Angiotensin-like peptide I (Fragment).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=96208932; PubMed=8829801;
RA   Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1308 MW;  CEF50DD761F2DB42 CRC64;


  Query Match            97.1%;  Score 34;  DB 1;  Length 10;
  Best Local Similarity  83.3%;  Pred. No. 0.16;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7


RESULT  13
ANGT_BOVIN
ID   ANGT_BOVIN     STANDARD;      PRT;    10 AA.
AC   P01017;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RA   Elliott D.F., Peart W.S.;
RT   "The amino acid sequence in a hypertensin.";
RL   Biochem. J. 65:246-254(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90345; A90345.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1282 MW;  CEEFBDD761F2DB42 CRC64;


  Query Match            97.1%;  Score 34;  DB 1;  Length 10;
  Best Local Similarity  83.3%;  Pred. No. 0.16;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7


RESULT  14
ANGT_CHICK
ID   ANGT_CHICK     STANDARD;      PRT;    10 AA.
AC   P01018;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken;
RX   MEDLINE=74127845; PubMed=4361802;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. 3. Structure of fowl
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 21:2085-2087(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=90284684; PubMed=2191893;
RA   Takei Y., Hasegawa Y.;
RT   "Vasopressor and depressor effects of native angiotensins and
RT   inhibition of these effects in the Japanese quail.";
RL   Gen. Comp. Endocrinol. 79:12-22(1990).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
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CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90917; A90917.
DR   PIR; A60624; A60624.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE      1     10       ANGIOTENSIN I.
FT   PEPTIDE      1      8       ANGIOTENSIN II.
FT   NON_TER     10     10
SQ   SEQUENCE   10 AA;  1232 MW;  CEFBEDD761F2DB42 CRC64;


  Query Match             97.1%;  Score 34;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 0.16;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           |||:||
Db       2 RVYVHP 7


RESULT  15
ANGT_CRIGE
ID   ANGT_CRIGE     STANDARD;      PRT;    11 AA.
AC   P09037;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Crinia-angiotensin II.
OS   Crinia georgiana (Quacking frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Crinia.
OX   NCBI_TaxID=8374;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE=80024575; PubMed=488254;
RA   Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT   "Amino acid composition and sequence of crinia-angiotensin, an
RT   angiotensin II-like endecapeptide from the skin of the Australian
RT   frog Crinia georgiana.";
RL   Experientia 35:1132-1133(1979).
DR   PIR; S07207; S07207.
KW   Vasoconstrictor.
SQ   SEQUENCE   11 AA;  1271 MW;  8A0921F7DB50440A CRC64;


  Query Match             94.3%;  Score 33;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 0.29;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           |:|:||
Db       5 RIYVHP 10


Search completed: July  1, 2002, 07:47:07
Job time: 473 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:10 ; Search time 122.73 Seconds
(without alignments)
8.457 Million cell updates/sec

Title: US-09-723-197-5
Perfect score: 35
Sequence: 1 RVYIHP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 35 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 2 | 35 | 100.0 | 245 | 6 | Q95J13 | Q95j13 pan troglod |
| 3 | 35 | 100.0 | 295 | 4 | Q9HA44 | Q9ha44 homo sapien |
| 4 | 35 | 100.0 | 436 | 11 | Q9CSJ0 | Q9csj0 mus musculu |
| 5 | 35 | 100.0 | 461 | 11 | Q9D2V0 | Q9d2v0 mus musculu |
| 6 | 35 | 100.0 | 477 | 4 | Q96FD5 | Q96fd5 homo sapien |
| 7 | 35 | 100.0 | 485 | 4 | Q96F91 | Q96f91 homo sapien |
| 8 | 35 | 100.0 | 485 | 6 | Q9GLP7 | Q9glp7 pan troglod |
| 9 | 35 | 100.0 | 485 | 6 | Q9GLP6 | Q9glp6 gorilla gor |
| 10 | 35 | 100.0 | 485 | 6 | Q9GLN8 | Q9gln8 pan troglod |
| 11 | 35 | 100.0 | 486 | 6 | Q9TSZ0 | Q9tsz0 callithrix |
| 12 | 35 | 100.0 | 533 | 4 | Q96SF7 | Q96sf7 homo sapien |
| 13 | 34 | 97.1 | 10 | 13 | Q9PS07 | Q9ps07 alligator m |
| 14 | 34 | 97.1 | 175 | 5 | Q9GQE4 | Q9gqe4 branchiosto |
| 15 | 34 | 97.1 | 183 | 5 | Q9GQE6 | Q9gqe6 branchiosto |
| 16 | 34 | 97.1 | 316 | 2 | Q9Z5B8 | Q9z5b8 streptomyce |
| 17 | 34 | 97.1 | 624 | 5 | Q966R5 | Q966r5 branchiosto |
| 18 | 33 | 94.3 | 249 | 13 | Q9W7Q1 | Q9w7q1 paralichthy |
| 19 | 33 | 94.3 | 694 | 2 | Q9EWA5 | Q9ewa5 streptomyce |
| 20 | 33 | 94.3 | 1094 | 2 | Q93H78 | Q93h78 streptomyce |
| 21 | 32 | 91.4 | 130 | 13 | Q90WR1 | Q90wr1 oryzias lat |
| 22 | 32 | 91.4 | 171 | 17 | Q971G2 | Q971g2 sulfolobus |
| 23 | 32 | 91.4 | 174 | 5 | Q9GQE7 | Q9gqe7 branchiosto |
| 24 | 32 | 91.4 | 179 | 5 | Q9GQE9 | Q9gqe9 branchiosto |
| 25 | 32 | 91.4 | 182 | 13 | O93357 | O93357 gallus gall |
| 26 | 32 | 91.4 | 194 | 13 | Q90WR0 | Q90wr0 oryzias lat |
| 27 | 32 | 91.4 | 290 | 11 | Q9D533 | Q9d533 mus musculu |
| 28 | 32 | 91.4 | 382 | 5 | Q9U3J6 | Q9u3j6 caenorhabdi |
| 29 | 32 | 91.4 | 382 | 13 | O73717 | O73717 gallus gall |
| 30 | 32 | 91.4 | 410 | 12 | Q99GP8 | Q99gp8 culex nigri |
| 31 | 32 | 91.4 | 420 | 5 | P90985 | P90985 caenorhabdi |
| 32 | 32 | 91.4 | 437 | 13 | Q9DDU4 | Q9ddu4 brachydanio |
| 33 | 32 | 91.4 | 580 | 12 | Q919R0 | Q919r0 culex nigri |
| 34 | 32 | 91.4 | 588 | 13 | Q9PVX4 | Q9pvx4 cynops pyrr |
| 35 | 32 | 91.4 | 591 | 13 | Q9PVX2 | Q9pvx2 cynops pyrr |
| 36 | 32 | 91.4 | 608 | 13 | Q9PVX3 | Q9pvx3 cynops pyrr |
| 37 | 32 | 91.4 | 672 | 13 | Q9W7B7 | Q9w7b7 brachydanio |
| 38 | 32 | 91.4 | 687 | 13 | Q9IAL0 | Q9ial0 brachydanio |
| 39 | 32 | 91.4 | 688 | 13 | Q9W7R7 | Q9w7r7 xenopus lae |
| 40 | 32 | 91.4 | 688 | 13 | Q9IBC8 | Q9ibc8 xenopus lae |
| 41 | 32 | 91.4 | 695 | 5 | Q9XUQ0 | Q9xuq0 caenorhabdi |
| 42 | 32 | 91.4 | 711 | 13 | Q9IBC7 | Q9ibc7 xenopus lae |
| 43 | 32 | 91.4 | 716 | 13 | Q9PUM1 | Q9pum1 xenopus lae |
| 44 | 32 | 91.4 | 808 | 5 | Q966Q2 | Q966q2 ciona intes |
| 45 | 31 | 88.6 | 87 | 13 | Q9PUS8 | Q9pus8 brachydanio |

ALIGNMENTS

RESULT 1
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 35; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYIHP 6

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          ||||||
Db      2 RVYIHP 7


RESULT   2
Q95J13
ID   Q95J13      PRELIMINARY;      PRT;   245 AA.
AC   Q95J13;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
GN   REN.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=504, AND 505;
RA   Satta Y.;
RT   "Comparison of DNA and protein polymorphims between humans and
RT   chimpanzees.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062027; BAB55856.1; -.
DR   EMBL; AB062028; BAB55857.1; -.
FT   NON_TER     245    245
SQ   SEQUENCE   245 AA;  26317 MW;  E0092390B9803E0B CRC64;


  Query Match             100.0%;  Score 35;  DB 6;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           ||||||
Db      35 RVYIHP 40


RESULT   3
Q9HA44
ID   Q9HA44      PRELIMINARY;      PRT;   295 AA.
AC   Q9HA44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE   TRANSCRIPTION FACTOR TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022330; BAB14014.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33197 MW;  F2BD3E53E0ED21E0 CRC64;


  Query Match             100.0%;  Score 35;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           ||||||
Db     171 RVYIHP 176


RESULT   4
Q9CSJ0
ID   Q9CSJ0      PRELIMINARY;      PRT;   436 AA.
AC   Q9CSJ0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2810012F10RIK PROTEIN (FRAGMENT).
GN   TBX18 OR 2810012F10RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012723; BAB28434.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:1923615; Tbx18.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   436 AA;  47478 MW;  8770E4F482CFC13A CRC64;


  Query Match             100.0%;  Score 35;  DB 11;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RVYIHP 6
           ||||||
Db      50 RVYIHP 55


RESULT   5
Q9D2V0
ID   Q9D2V0      PRELIMINARY;      PRT;   461 AA.
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AC   Q9D2V0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018763; BAB31393.1; -.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
SQ   SEQUENCE   461 AA;  50327 MW;  446EB0881079251F CRC64;


  Query Match           100.0%;  Score 35;  DB 11;  Length 461;
  Best Local Similarity  100.0%;  Pred. No. 30;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     31 RVYIHP 36


RESULT   6
Q96FD5
ID   Q96FD5      PRELIMINARY;      PRT;   477 AA.
AC   Q96FD5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SIMILAR TO ANGIOTENSINOGEN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011231; AAH11231.1; -.
SQ   SEQUENCE   477 AA;  51985 MW;  AB79B8B70592FDE2 CRC64;


  Query Match           100.0%;  Score 35;  DB 4;  Length 477;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     26 RVYIHP 31


RESULT   7
Q96F91
ID   Q96F91      PRELIMINARY;      PRT;   485 AA.
AC   Q96F91;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE
DE   A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 8).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011519; AAH11519.1; -.
SQ   SEQUENCE   485 AA;  53114 MW;  50BA5E9DCD4C8E7F CRC64;


  Query Match           100.0%;  Score 35;  DB 4;  Length 485;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT   8
Q9GLP7
ID   Q9GLP7      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188487; AAG29056.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53140 MW;  49EFB54AF31F8ADC CRC64;


  Query Match           100.0%;  Score 35;  DB 6;  Length 485;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT   9
Q9GLP6
ID   Q9GLP6      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188488; AAG29057.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53186 MW;  53BC9235271C8255 CRC64;


  Query Match             100.0%;  Score 35;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT  10
Q9GLN8
ID   Q9GLN8      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLN8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20469400; PubMed=11013071;
RA   Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA   Jeunemaitre X.;
RT   "Human-Chimpanzee DNA sequence variation in the four major genes of
RT   the renin angiotensin system.";
RL   Genomics 69:14-26(2000).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF193461; AAG30306.1; -.
DR   EMBL; AF193458; AAG30306.1; JOINED.
DR   EMBL; AF193459; AAG30306.1; JOINED.
DR   EMBL; AF193460; AAG30306.1; JOINED.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53110 MW;  C14C67E49A53F05F CRC64;


  Query Match             100.0%;  Score 35;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT  11
Q9TSZ0
ID   Q9TSZ0      PRELIMINARY;      PRT;   486 AA.
AC   Q9TSZ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR.
GN   ANGT.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065005; PubMed=10598135;
RA   Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;
RT   "Cloning and characterization of marmoset renin: comparison with human
RT   renin.";
RL   J. Cardiovasc. Pharmacol. 34:893-897(1999).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AJ132343; CAB64880.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin; Signal.
FT   SIGNAL        1     33       POTENTIAL.
FT   CHAIN        34    486       ANGIOTENSINOGEN.
SQ   SEQUENCE   486 AA;  53374 MW;  5408129B2F71FB8B CRC64;


  Query Match             100.0%;  Score 35;  DB 6;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db     35 RVYIHP 40


RESULT  12
Q96SF7
ID   Q96SF7      PRELIMINARY;      PRT;   533 AA.
AC   Q96SF7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DJ794L19.1 (NOVEL T-BOX (TBX) FAMILY MEMBER) (FRAGMENT).
GN   DJ794L19.1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   SEQUENCE FROM N.A.
RA   Cobley V.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL357045; CAC39400.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   533 AA;  58308 MW;  7ECC5008CEE275A9 CRC64;


  Query Match             100.0%;  Score 35;  DB 4;  Length 533;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          ||||||
Db    126 RVYIHP 131


RESULT  13
Q9PS07
ID   Q9PS07      PRELIMINARY;      PRT;    10 AA.
AC   Q9PS07;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ANGIOTENSIN I, ANG I.
OS   Alligator mississippiensis (American alligator).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX   NCBI_TaxID=8496;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93307610; PubMed=8319878;
RA   Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA   Stephens G.A., Sakakibara S.;
RT   "New angiotensin I isolated from a reptile, Alligator
RT   mississippiensis.";
RL   Gen. Comp. Endocrinol. 90:214-219(1993).
SQ   SEQUENCE   10 AA;  1216 MW;  CEE38DD761F2DB42 CRC64;


  Query Match             97.1%;  Score 34;  DB 13;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 1.1;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          |||:||
Db      2 RVYVHP 7


RESULT  14
Q9GQE4
ID   Q9GQE4      PRELIMINARY;      PRT;   175 AA.
AC   Q9GQE4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T-BOX PROTEIN AMPHIEOMES/TBR1/TBX21 (FRAGMENT).
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20519458; PubMed=11063699;
RA   Ruvinsky I., Silver L.M., Gibson-Brown J.J.;
RT   "Phylogenetic analysis of T-Box genes demonstrates the importance of
RT   amphioxus for understanding evolution of the vertebrate genome.";
RL   Genetics 156:1249-1257(2000).
DR   EMBL; AF262568; AAG34893.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
FT   NON_TER       1      1
FT   NON_TER     175    175
SQ   SEQUENCE   175 AA;  20057 MW;  95D34C4996A0DD6B CRC64;


  Query Match             97.1%;  Score 34;  DB 5;  Length 175;
  Best Local Similarity   83.3%;  Pred. No. 19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          |||:||
Db     73 RVYVHP 78


RESULT  15
Q9GQE6
ID   Q9GQE6      PRELIMINARY;      PRT;   183 AA.
AC   Q9GQE6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T-BOX PROTEIN AMPHITBX15/18/22 (FRAGMENT).
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20519458; PubMed=11063699;
RA   Ruvinsky I., Silver L.M., Gibson-Brown J.J.;
RT   "Phylogenetic analysis of T-Box genes demonstrates the importance of
RT   amphioxus for understanding evolution of the vertebrate genome.";
RL   Genetics 156:1249-1257(2000).
DR   EMBL; AF262566; AAG34891.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
FT   NON_TER       1      1
FT   NON_TER     183    183
SQ   SEQUENCE   183 AA;  21027 MW;  F01E0579067071FD CRC64;


  Query Match             97.1%;  Score 34;  DB 5;  Length 183;
  Best Local Similarity   83.3%;  Pred. No. 19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RVYIHP 6
          |||:||
Db     74 RVYVHP 79


Search completed: July  1, 2002, 07:45:11
Job time: 407 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds
(without alignments)
3.509 Million cell updates/sec

Title: US-09-723-197-6
Perfect score: 30
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 30 | 100.0 | 5 | 17 | AAR95667 | Angiotensin II fra |
| 2 | 30 | 100.0 | 5 | 18 | AAW33326 | Targetting conjuga |
| 3 | 30 | 100.0 | 5 | 18 | AAW33018 | Targetting conjuga |
| 4 | 30 | 100.0 | 5 | 18 | AAW11210 | Targetting conjuga |
| 5 | 30 | 100.0 | 5 | 18 | AAW14984 | Conjugating peptid |
| 6 | 30 | 100.0 | 5 | 19 | AAW65602 | Angiotensin II ana |
| 7 | 30 | 100.0 | 5 | 19 | AAW64733 | Angiotensin II pep |
| 8 | 30 | 100.0 | 5 | 19 | AAW71115 | Peptide AII(3-7) u |
| 9 | 30 | 100.0 | 5 | 20 | AAY49591 | Angiotensin analog |
| 10 | 30 | 100.0 | 5 | 20 | AAY33906 | Angiotensin II ana |
| 11 | 30 | 100.0 | 5 | 20 | AAY30544 | Amino acid sequenc |
| 12 | 30 | 100.0 | 5 | 20 | AAY30588 | Amino acid sequenc |
| 13 | 30 | 100.0 | 5 | 20 | AAY32719 | Angiotensin II ana |
| 14 | 30 | 100.0 | 5 | 20 | AAY33773 | Angiotensin II (AI |
| 15 | 30 | 100.0 | 5 | 20 | AAY15350 | Angiotensin II (AI |
| 16 | 30 | 100.0 | 5 | 20 | AAY15310 | Angiotensin II (AI |
| 17 | 30 | 100.0 | 5 | 21 | AAB27406 | Angiotensin II ana |
| 18 | 30 | 100.0 | 5 | 21 | AAB28104 | Angiotensin II ana |
| 19 | 30 | 100.0 | 5 | 21 | AAY84129 | Peptide comprising |
| 20 | 30 | 100.0 | 5 | 21 | AAY77042 | Angiotensin II (AI |
| 21 | 30 | 100.0 | 5 | 21 | AAY57406 | Angiotensin peptid |
| 22 | 30 | 100.0 | 5 | 22 | AAE08876 | AII peptide (resid |
| 23 | 30 | 100.0 | 5 | 22 | AAE02993 | Human angiotensin |
| 24 | 30 | 100.0 | 5 | 22 | AAE03156 | Human angiotensin |
| 25 | 30 | 100.0 | 6 | 17 | AAR95664 | Angiotensin II fra |
| 26 | 30 | 100.0 | 6 | 17 | AAR95666 | Angiotensin II fra |
| 27 | 30 | 100.0 | 6 | 18 | AAW33325 | Targetting conjuga |
| 28 | 30 | 100.0 | 6 | 18 | AAW32605 | Angiotensin IV ant |
| 29 | 30 | 100.0 | 6 | 18 | AAW32609 | D-Val1-Angiotensin |
| 30 | 30 | 100.0 | 6 | 18 | AAW33017 | Targetting conjuga |
| 31 | 30 | 100.0 | 6 | 18 | AAW11209 | Targetting conjuga |
| 32 | 30 | 100.0 | 6 | 18 | AAW14983 | Conjugating peptid |
| 33 | 30 | 100.0 | 6 | 18 | AAW14124 | Angiotensin IV ant |
| 34 | 30 | 100.0 | 6 | 19 | AAW65599 | Angiotensin II ana |
| 35 | 30 | 100.0 | 6 | 19 | AAW65601 | Angiotensin II ana |
| 36 | 30 | 100.0 | 6 | 19 | AAW64730 | Angiotensin II pep |
| 37 | 30 | 100.0 | 6 | 19 | AAW64732 | Angiotensin II pep |
| 38 | 30 | 100.0 | 6 | 19 | AAW71112 | Peptide AII(3-8) u |
| 39 | 30 | 100.0 | 6 | 19 | AAW71114 | Peptide AII(2-7) u |
| 40 | 30 | 100.0 | 6 | 19 | AAW65540 | Peptide motif havi |
| 41 | 30 | 100.0 | 6 | 20 | AAY49588 | Angiotensin analog |
| 42 | 30 | 100.0 | 6 | 20 | AAY49590 | Angiotensin analog |
| 43 | 30 | 100.0 | 6 | 20 | AAY50297 | Neutrophil-activat |
| 44 | 30 | 100.0 | 6 | 20 | AAY33903 | Angiotensin II ana |
| 45 | 30 | 100.0 | 6 | 20 | AAY33905 | Angiotensin II ana |

ALIGNMENTS

RESULT 1
AAR95667
ID AAR95667 standard; peptide; 5 AA.
XX
AC AAR95667;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(3-7).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 2
AAW33326
ID AAW33326 standard; peptide; 5 AA.
XX
AC AAW33326;
XX
DT 05-FEB-1998 (first entry)
XX
DE Targetting conjugate for bis-nicotinamide bifunctional chelator.
XX
KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;
KW rhenium; conjugate; endothelin; angiotensin; targetting agent;
KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
KW delivery.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9710853-A2.
XX
PD 27-MAR-1997.
XX
PF 19-SEP-1996; 96WO-DE01824.
XX
PR 21-SEP-1995; 95DE-4036783.
XX
PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
XX
PI Dinkelborg L, Hilger CS, Kramp W, Platzek J;
PI Raduechel B;
XX
DR WPI; 1997-212562/19.
XX
PT New bis-nicotinamide bi:functional chelating agents - forming new,
PT stable technetium or rhenium complexes and conjugates useful as
PT radiodiagnostic and radio:therapeutic agents
XX
PS Claim 11; Page 42; 47pp; German.
XX
CC Novel bis-nicotinamide bifunctional chelating agent for radioactive
CC technetium and rhenium, when conjugated to an endothelin or
CC angiotensin derived targetting agent, e.g. the present peptide, can
CC be used for the in vivo imaging of organs, receptors and receptor
CC containing tissues and/or atherosclerotic plaques, e.g. for the
CC diagnosis of breast or prostatic carcinoma. They can also be used
CC for cytostatic agent delivery.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 3
AAW33018
ID AAW33018 standard; peptide; 5 AA.
XX
AC AAW33018;
XX
DT 26-JAN-1998 (first entry)
XX
DE Targetting conjugate for bifunctional sulphonamide type ligand.
XX
KW Bifunctional sulphonamide; ligand; radioactive; technetium;
KW rhenium; conjugate; endothelin; angiotensin; targetting agent;
KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
KW delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN DE19536785-A1.
XX
PD 27-MAR-1997.
XX
PF 21-SEP-1995; 95DE-1036785.
XX
PR 21-SEP-1995; 95DE-1036785.
XX
PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
XX
PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
PI Raduechel B;
XX
DR WPI; 1997-193894/18.
XX
PT Bifunctional sulphonamide type ligands for radioactive technetium or
PT rhenium - and their chelates and conjugates, useful for imaging
PT carcinoma or atherosclerosis
XX
PS Claim 9; Page 12; 12pp; German.
XX
CC Novel bifunctional sulphonamide type ligands for radioactive
CC technetium and rhenium, when conjugated to an endothelin or
CC angiotensin derived targetting agent, e.g. the present peptide, can
CC be used for the in vivo imaging of organs, receptors and receptor
CC containing tissues and/or atherosclerotic plaques, e.g. for the
CC diagnosis of breast or prostatic carcinoma. They can also be used
CC for cytostatic agent delivery.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 4
AAW11210
ID AAW11210 standard; peptide; 5 AA.
XX
AC AAW11210;
XX
DT 26-JAN-1998 (first entry)
XX
DE Targetting conjugate for bifunctional sulphonamide type ligand.
XX
KW Bifunctional sulphonamide; ligand; radioactive; technetium;
KW rhenium; conjugate; endothelin; angiotensin; targetting agent;
KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
KW delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN DE19536780-A1.
XX
PD 27-MAR-1997.
XX
PF 21-SEP-1995; 95DE-1036780.
XX
PR 21-SEP-1995; 95DE-1036780.
XX
PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
XX
PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
PI Raduechel B;
XX
DR WPI; 1997-193892/18.
XX
PT Bifunctional sulphonamide type ligands for radioactive technetium
PT and rhenium - and their chelates and conjugates with targetting
PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.
XX
PS Claim 11; Page 19; 19pp; German.
XX
CC Novel bifunctional sulphonamide type ligands for radioactive
CC technetium and rhenium, when conjugated to an endothelin or
CC angiotensin derived targetting agent, e.g. the present peptide, can
CC be used for the in vivo imaging of organs, receptors and receptor
CC containing tissues and/or atherosclerotic plaques, e.g. for the
CC diagnosis of breast or prostatic carcinoma. They can also be used
CC for cytostatic agent delivery.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 5
AAW14984
ID AAW14984 standard; peptide; 5 AA.
XX
AC AAW14984;
XX
DT 28-NOV-1997 (first entry)
XX
DE Conjugating peptide for radio-therapeutic/diagnostic agent.
XX
KW Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;
KW radiodiagnostic; radiotherapeutic; diagnosis; tumour; ischaemia;
KW atherosclerosis; vascular disorder; ischemia.
XX
OS Synthetic.
XX
PN WO9710852-A2.
XX
PD 27-MAR-1997.
XX
PF 19-SEP-1996; 96WO-DE01821.
XX
PR 21-SEP-1995; 95DE-4036781.
XX
PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
XX
PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
PI Raduechel B;
XX
DR WPI; 1997-202627/18.
XX
PT New sulphide-sulphonamide bi:functional chelating agents - forming
PT new, stable technetium or rhenium complexes and conjugates useful as
PT radiodiagnostic and radio-therapeutic agents
XX
PS Claim 13; Page 45; 50pp; German.
XX
CC XSNS-type bifunctional sulphide containing sulphonamide chelating
CC agents and their technetium or rhenium complexes, can form
CC covalently bonded conjugates with substances selectively enriched
CC in diseased tissue, e.g. the present peptide. The substance is an
CC endothelin or angiotensin peptide, or a partial sequence, analogue,
CC derivative or antagonist, or a chemotactic peptide.
CC The conjugates are radiodiagnostic or radiotherapeutic agents,
CC useful in the diagnosis of tumours, ischaemia or atherosclerotic
CC vascular disorders.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 6
AAW65602
ID AAW65602 standard; peptide; 5 AA.
XX
AC AAW65602;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(3-7).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX

PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 7
AAW64733
ID AAW64733 standard; peptide; 5 AA.
XX
AC AAW64733;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #5.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI dizerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 8
AAW71115
ID AAW71115 standard; peptide; 5 AA.
XX
AC AAW71115;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(3-7) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.

XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 9
AAY49591
ID AAY49591 standard; peptide; 5 AA.
XX
AC AAY49591;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:6.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 1 vyihp 5

RESULT 10
AAY33906
ID AAY33906 standard; peptide; 5 AA.
XX
AC AAY33906;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(3-7).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(3-7). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments, or AII
CC AT2 type 2 receptor agonists can rapidly provide a large population of
CC ESCs (Embryonic Stem Cell) for use in replacement therapy. Similarly,
CC methods that increase in vivo proliferation of ESCs will enhance the

```
CC   utility of replacement therapy by rapidly increasing local concentration
CC    of the stem cells and their progeny at the site of therapy.
CC   The method also increases the potential utility of ESCs as vehicles for
CC   gene therapy in certain disorders by more efficiently providing a large
CC   number of such cells for transfection, and also by providing a more
CC   efficient means to rapidly expand transfected ESCs.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 30;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 vyihp 5


RESULT  11
AAY30544
ID   AAY30544 standard; peptide; 5 AA.
XX
AC   AAY30544;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII3-7.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents  -
XX
PS   Claim 2; Page 54; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 30;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 vyihp 5


RESULT  12
AAY30588
ID   AAY30588 standard; peptide; 5 AA.
XX
AC   AAY30588;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII3-7.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
KW   gene therapy; hematopoietic disorder.
XX
OS   Synthetic.
XX
PN   WO9945945-A1.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05194.
XX
PR   10-MAR-1998;   98US-0077382.
PR   09-APR-1998;   98US-0081262.
PR   30-APR-1998;   98US-0083670.
PR   19-JUN-1998;   98US-0090096.
PR   22-JUN-1998;   98US-0090216.
PR   11-SEP-1998;   98US-0099957.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA   (RODG/) RODGERS K E.
PA   (DIZE/) DIZEREGA G.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551209/46.
XX
PT   Use of angiotensin and angiotensin type peptides, for mitigating
PT   radiation induced tissue damage, improving bone marrow transplantation
PT   and promoting megakaryocyte and platelet production  -
XX
PS   Claim 2; Page 87; 116pp; English.
XX
CC   AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes a method for mitigating
CC   radiation induced tissue damage, improving the effectiveness of
CC   radiation therapy, to support bone marrow transplantation, and
CC   promoting megakaryocyte production and mobilization and platelet
CC   production. The method comprises administration of the present peptides.
CC   The methods can be used to mitigate radiation induced tissue damage, to
CC   improve the effectiveness of radiation therapy, to support bone marrow
CC   transplantation, and to promote megakaryocyte production and
CC   mobilization and platelet production. They are used particularly in
CC   cancer therapy. They can also be used to provide megakaryocytes as
CC   vehicles for gene therapy in hematopoietic disorders, by providing a
CC   more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 30;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
```

```
          |||||
Db        1 vyihp 5


RESULT  13
AAY32719
ID   AAY32719 standard; peptide; 5 AA.
XX
AC   AAY32719;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Angiotensin II analogue AII(3-7).
XX
KW   Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW   chemotaxis; growth factor; liver regeneration; cirrhosis;
KW   hepatocarcinoma; hepatectomy; transplantation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9939743-A2.
XX
PD   12-AUG-1999.
XX
PF   08-FEB-1999;   99WO-US02618.
XX
PR   13-NOV-1998;   98US-0108412.
PR   09-FEB-1998;   98US-0074104.
XX
PA   (DIZE/) DIZEREGA G.
PA   (RODG/) RODGERS K E.
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Dizerega G,  Rodgers KE;
XX
DR   WPI; 1999-508461/42.
XX
PT   Hepatic cell proliferation with angiotensin I and II derived active
PT   agents, useful for regeneration of liver after resection
XX
PS   Claim 2; Page 9; 66pp; English.
XX
CC   Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC   peptides are derived from the AII peptide (AAY32750). AII increases
CC   mitogenesis and chemotaxis in cultured cells, and also increases the
CC   release of growth factors and extracellular matrices. AII has also been
CC   shown to increase the proliferation of certain cell types. The AII
CC   analogue peptides can be used as the active agent in a method for
CC   promoting hepatic cell proliferation and differentiation. The method
CC   involves contacting the hepatic cells with an amount effective enough to
CC   promote proliferation of any of the peptides. This method is useful in
CC   liver regeneration following resection of hepatocarcinomas, hepatitis
CC   infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC   failure, hepatocyte transplantation, liver transplantation and other
CC   hepatic disorders where rapid regeneration of the liver is desirable. The
CC   methods are also useful in rapidly providing a large population of
CC   hepatic cells for use in cell therapy and for providing a large
CC   population of transfected hepatic cells for use in gene therapy.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 30;  DB 20;  Length 5;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 vyihp 5


RESULT  14
AAY33773
ID   AAY33773 standard; peptide; 5 AA.
XX
AC   AAY33773;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Angiotensin II (AII) octapeptide fragment AII(3-7).
XX
KW   Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW   neuronal cell proliferation; differentiation; Alzheimer's disease;
KW   Parkinson's disease; neuron replacement therapy.
XX
OS   Homo sapiens.
XX
PN   WO9942123-A1.
XX
PD   26-AUG-1999.
XX
PF   19-FEB-1999;   99WO-US03772.
XX
PR   19-FEB-1998;   98US-0075232.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Dizerega G,  Rodgers KE;
XX
DR   WPI; 1999-527420/44.
XX
PT   Promoting neuronal cell proliferation and differentiation
XX
PS   Claim 2; Page 10; 62pp; English.
XX
CC   Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC   II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC   application of angiotensin to wound tissue significantly increases the
CC   rate of wound healing. AII is known to increase mitogenesis and
CC   chemotaxis in cultured cells, and also increases their release of growth
CC   factors and extracellular matrices, implicating it in cell growth and
CC   differentiation. AT2 receptors are receptors for AII and are thought to
CC   be involved in the mediation of the cell differentiation effects of AII.
CC   Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC   cell proliferation or differentiation. This method is useful in the
CC   treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC   therapy.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 30;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 vyihp 5


RESULT  15
AAY15350
ID   AAY15350 standard; peptide; 5 AA.
XX
AC   AAY15350;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Angiotensin II (AII) analogue, AII(3-7).
XX
KW   burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW   AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS   Synthetic.
OS   Homo sapiens.
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XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX
PS Claim 2; Page 9; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 VYIHP 5
          |||||
Db      1 vyihp 5
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Search completed: July 1, 2002, 07:41:55
Job time: 347 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds
(without alignments)
2.066 Million cell updates/sec

Title: US-09-723-197-6
Perfect score: 30
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 30 | 100.0 | 5 | 2 | US-08-360-784B-27 | Sequence 27, Appl |
| 2 | 30 | 100.0 | 5 | 2 | US-08-465-775-6 | Sequence 6, Appli |
| 3 | 30 | 100.0 | 5 | 3 | US-09-054-308A-27 | Sequence 27, Appl |
| 4 | 30 | 100.0 | 5 | 3 | US-09-208-337-6 | Sequence 6, Appli |
| 5 | 30 | 100.0 | 5 | 3 | US-08-990-664-7 | Sequence 7, Appli |
| 6 | 30 | 100.0 | 5 | 4 | US-09-373-962-6 | Sequence 6, Appli |
| 7 | 30 | 100.0 | 5 | 4 | US-09-245-680-6 | Sequence 6, Appli |
| 8 | 30 | 100.0 | 5 | 4 | US-09-198-806C-6 | Sequence 6, Appli |
| 9 | 30 | 100.0 | 5 | 4 | US-09-352-191-6 | Sequence 6, Appli |
| 10 | 30 | 100.0 | 5 | 4 | US-09-012-400-6 | Sequence 6, Appli |
| 11 | 30 | 100.0 | 6 | 1 | US-08-113-292A-2 | Sequence 2, Appli |
| 12 | 30 | 100.0 | 6 | 2 | US-08-360-784B-1 | Sequence 1, Appli |
| 13 | 30 | 100.0 | 6 | 2 | US-08-360-784B-37 | Sequence 37, Appl |
| 14 | 30 | 100.0 | 6 | 2 | US-08-465-775-3 | Sequence 3, Appli |
| 15 | 30 | 100.0 | 6 | 2 | US-08-465-775-5 | Sequence 5, Appli |
| 16 | 30 | 100.0 | 6 | 3 | US-09-054-308A-1 | Sequence 1, Appli |
| 17 | 30 | 100.0 | 6 | 3 | US-09-054-308A-37 | Sequence 37, Appl |
| 18 | 30 | 100.0 | 6 | 3 | US-09-208-337-3 | Sequence 3, Appli |
| 19 | 30 | 100.0 | 6 | 3 | US-09-208-337-5 | Sequence 5, Appli |
| 20 | 30 | 100.0 | 6 | 3 | US-08-990-664-4 | Sequence 4, Appli |
| 21 | 30 | 100.0 | 6 | 3 | US-08-990-664-6 | Sequence 6, Appli |
| 22 | 30 | 100.0 | 6 | 4 | US-09-373-962-3 | Sequence 3, Appli |
| 23 | 30 | 100.0 | 6 | 4 | US-09-373-962-5 | Sequence 5, Appli |
| 24 | 30 | 100.0 | 6 | 4 | US-09-245-680-3 | Sequence 3, Appli |
| 25 | 30 | 100.0 | 6 | 4 | US-09-245-680-5 | Sequence 5, Appli |
| 26 | 30 | 100.0 | 6 | 4 | US-09-198-806C-3 | Sequence 3, Appli |
| 27 | 30 | 100.0 | 6 | 4 | US-09-198-806C-5 | Sequence 5, Appli |
| 28 | 30 | 100.0 | 6 | 4 | US-09-352-191-3 | Sequence 3, Appli |
| 29 | 30 | 100.0 | 6 | 4 | US-09-352-191-5 | Sequence 5, Appli |
| 30 | 30 | 100.0 | 6 | 4 | US-09-012-400-3 | Sequence 3, Appli |
| 31 | 30 | 100.0 | 6 | 4 | US-09-012-400-5 | Sequence 5, Appli |
| 32 | 30 | 100.0 | 7 | 1 | US-08-021-839A-4 | Sequence 4, Appli |
| 33 | 30 | 100.0 | 7 | 1 | US-07-776-272-3 | Sequence 3, Appli |
| 34 | 30 | 100.0 | 7 | 1 | US-08-337-781-3 | Sequence 3, Appli |
| 35 | 30 | 100.0 | 7 | 2 | US-08-115-968-6 | Sequence 6, Appli |
| 36 | 30 | 100.0 | 7 | 2 | US-08-115-968-9 | Sequence 9, Appli |
| 37 | 30 | 100.0 | 7 | 2 | US-08-115-968-10 | Sequence 10, Appl |
| 38 | 30 | 100.0 | 7 | 2 | US-08-115-968-11 | Sequence 11, Appl |
| 39 | 30 | 100.0 | 7 | 2 | US-08-115-968-12 | Sequence 12, Appl |
| 40 | 30 | 100.0 | 7 | 2 | US-08-115-968-13 | Sequence 13, Appl |
| 41 | 30 | 100.0 | 7 | 2 | US-08-115-968-14 | Sequence 14, Appl |
| 42 | 30 | 100.0 | 7 | 2 | US-08-115-968-15 | Sequence 15, Appl |
| 43 | 30 | 100.0 | 7 | 2 | US-08-115-968-16 | Sequence 16, Appl |
| 44 | 30 | 100.0 | 7 | 2 | US-08-360-784B-3 | Sequence 3, Appli |
| 45 | 30 | 100.0 | 7 | 2 | US-08-360-784B-8 | Sequence 8, Appli |

ALIGNMENTS

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RESULT   1
US-08-360-784B-27
; Sequence 27, Application US/08360784B
; Patent No. 5854388
;  GENERAL INFORMATION:
;    APPLICANT:  Harding, J.W.
;    APPLICANT:  Wright, J.W.
;    TITLE OF INVENTION:  Angiotensin IV Peptides and Receptor
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson & Kindness
;      STREET:  1420 Fifth Ave., Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,784B
;      FILING DATE:  22-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sheiness, Diana K..
;      REGISTRATION NUMBER:  35,356
;      REFERENCE/DOCKET NUMBER:  WSUR-1-8113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 224-0735
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bos taurus
US-08-360-784B-27


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db      1 VYIHP 5


RESULT   2
US-08-465-775-6
; Sequence 6, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-6


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Qy      1 VYIHP 5
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Db      1 VYIHP 5


RESULT   3
US-09-054-308A-27
; Sequence 27, Application US/09054308A
; Patent No. 6022696
;  GENERAL INFORMATION:
;    APPLICANT:  Harding, J.W.
;    APPLICANT:  Wright, J.W.
;    TITLE OF INVENTION:  Angiotensin IV Peptides and Receptor
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson & Kindness
;      STREET:  1420 Fifth Ave., Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,308A
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,784
;      FILING DATE:  22-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shelton, Dennis K.
;      REGISTRATION NUMBER:  26,997
;      REFERENCE/DOCKET NUMBER:  WSUR110660
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 224-0718
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bos taurus
US-09-054-308A-27


  Query Match           100.0%;  Score 30;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT   4
US-09-208-337-6
; Sequence 6, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
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;       APPLICATION NUMBER:  08/337,781
;       FILING DATE:  14-NOV-1994
;       APPLICATION NUMBER:  08/126,368
;       FILING DATE:  24-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Altman, Daniel E
;       REGISTRATION NUMBER:  34,115
;       REFERENCE/DOCKET NUMBER:  USC010.001CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  949-760-0404
;       TELEFAX:  949-760-9502
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Peptide
US-09-208-337-6


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Qy      1 VYIHP 5
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Db      1 VYIHP 5


RESULT   5
US-08-990-664-7
; Sequence 7, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;     APPLICANT:  Rodgers, Kathleen
;     APPLICANT:  diZerega, Gere
;     TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;     TITLE OF INVENTION:  IN SKIN GRAFTS
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Knobbe, Martens, Olson & Bear
;       STREET:  620 Newport Center Drive  16th Floor
;       CITY:  Newport Beach
;       STATE:  CA
;       COUNTRY:  U.S.A.
;       ZIP:  92660
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/990,664
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,310
;       FILING DATE:  16-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Altman, Daniel E
;       REGISTRATION NUMBER:  34,115
;       REFERENCE/DOCKET NUMBER:  USC012.001A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  714-760-0404
;       TELEFAX:  714-760-9502
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-990-664-7


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Qy      1 VYIHP 5
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Db      1 VYIHP 5


RESULT   6
US-09-373-962-6
; Sequence 6, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (3-7)
US-09-373-962-6


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Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT   7
US-09-245-680-6
; Sequence 6, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (3-7)
US-09-245-680-6


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Qy      1 VYIHP 5
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Db      1 VYIHP 5


RESULT   8
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; Sequence 6, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (3-7)
US-09-198-806C-6


  Query Match            100.0%;  Score 30;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
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Db      1 VYIHP 5


RESULT   9
US-09-352-191-6
; Sequence 6, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (3-7)
US-09-352-191-6


  Query Match            100.0%;  Score 30;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  10
US-09-012-400-6
; Sequence 6, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (3-7)
US-09-012-400-6


  Query Match            100.0%;  Score 30;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  11
US-08-113-292A-2
; Sequence 2, Application US/08113292A
; Patent No. 5599663
;  GENERAL INFORMATION:
;    APPLICANT:  Robert E. Vaughan
;    TITLE OF INVENTION:  ANGIOTENSIN IV AND ANALOGS AS
;    TITLE OF INVENTION:  REGULATORS OF FIBRINOLYSIS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/113,292A
;      FILING DATE:  August 27, 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John W. Freeman
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  05311/005001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6
;      TYPE:  amino acid
;      STRANDEDNESS:  N/A
;      TOPOLOGY:  linear
US-08-113-292A-2


  Query Match            100.0%;  Score 30;  DB 1;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  12
US-08-360-784B-1
; Sequence 1, Application US/08360784B
; Patent No. 5854388
;  GENERAL INFORMATION:
;    APPLICANT:  Harding, J.W.
;    APPLICANT:  Wright, J.W.
;    TITLE OF INVENTION:  Angiotensin IV Peptides and Receptor
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson & Kindness
;      STREET:  1420 Fifth Ave., Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,784B
;      FILING DATE:  22-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sheiness, Diana K..
;      REGISTRATION NUMBER:  35,356
;      REFERENCE/DOCKET NUMBER:  WSUR-1-8113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 224-0735
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;      DESCRIPTION:  Angiotensin IV
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bos taurus
US-08-360-784B-1


  Query Match             100.0%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  13
US-08-360-784B-37
; Sequence 37, Application US/08360784B
; Patent No. 5854388
;  GENERAL INFORMATION:
;    APPLICANT:  Harding, J.W.
;    APPLICANT:  Wright, J.W.
;    TITLE OF INVENTION:  Angiotensin IV Peptides and Receptor
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen O'Connor Johnson & Kindness
;      STREET:  1420 Fifth Ave., Suite 2800
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,784B
;      FILING DATE:  22-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sheiness, Diana K..
;      REGISTRATION NUMBER:  35,356
;      REFERENCE/DOCKET NUMBER:  WSUR-1-8113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 224-0735
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Bos taurus
US-08-360-784B-37


  Query Match             100.0%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  14
US-08-465-775-3
; Sequence 3, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-3


  Query Match             100.0%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      1 VYIHP 5


RESULT  15
US-08-465-775-5
; Sequence 5, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-5


  Query Match             100.0%;  Score 30;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      2 VYIHP 6


Search completed: July  1, 2002, 07:43:00
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:28 ; Search time 69.93 Seconds
(without alignments)
6.870 Million cell updates/sec

Title: US-09-723-197-6
Perfect score: 30
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 30 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 2 | 30 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 3 | 30 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 4 | 30 | 100.0 | 177 | 2 | C71329 | hypothetical prote |
| 5 | 30 | 100.0 | 184 | 2 | AC1584 | hypothetical prote |
| 6 | 30 | 100.0 | 349 | 2 | T50372 | probable ATP-depen |
| 7 | 30 | 100.0 | 385 | 2 | G84459 | probable GDP-manno |
| 8 | 30 | 100.0 | 415 | 2 | G96778 | hypothetical prote |
| 9 | 30 | 100.0 | 423 | 1 | A49125 | gastrulation regul |
| 10 | 30 | 100.0 | 432 | 1 | A41056 | brachyury homolog |
| 11 | 30 | 100.0 | 436 | 1 | S08156 | gene T protein - m |
| 12 | 30 | 100.0 | 444 | 2 | T20803 | hypothetical prote |
| 13 | 30 | 100.0 | 476 | 1 | JC2318 | angiotensin precur |
| 14 | 30 | 100.0 | 477 | 1 | ANRT | angiotensin precur |
| 15 | 30 | 100.0 | 477 | 1 | A29978 | angiotensin precur |
| 16 | 30 | 100.0 | 485 | 1 | ANHU | angiotensin precur |
| 17 | 30 | 100.0 | 540 | 2 | S72233 | transcription fact |
| 18 | 30 | 100.0 | 678 | 2 | S14173 | SIR1 protein - yea |
| 19 | 30 | 100.0 | 695 | 2 | T24950 | hypothetical prote |
| 20 | 30 | 100.0 | 759 | 2 | AF0577 | molybdopterin-cont |
| 21 | 30 | 100.0 | 968 | 2 | T46568 | ATP-dependent RNA |
| 22 | 30 | 100.0 | 980 | 2 | T39630 | valine-tRNA ligase |
| 23 | 30 | 100.0 | 982 | 2 | T04542 | hypothetical prote |
| 24 | 30 | 100.0 | 1200 | 2 | T15921 | hypothetical prote |
| 25 | 30 | 100.0 | 1220 | 2 | A56236 | probable RNA helic |
| 26 | 30 | 100.0 | 1267 | 2 | S53058 | probable membrane |
| 27 | 30 | 100.0 | 1355 | 1 | VGBEI1 | 149K glycoprotein |
| 28 | 29 | 96.7 | 10 | 2 | A60624 | angiotensin I - Ja |
| 29 | 29 | 96.7 | 10 | 2 | A90917 | angiotensin precur |
| 30 | 29 | 96.7 | 10 | 2 | A90345 | angiotensin precur |
| 31 | 29 | 96.7 | 18 | 4 | I39461 | anti-angiotensin, |
| 32 | 29 | 96.7 | 141 | 2 | JQ1669 | hypothetical 16.1K |
| 33 | 29 | 96.7 | 171 | 2 | AE0670 | probable acetyltra |
| 34 | 29 | 96.7 | 172 | 1 | C64897 | probable phosphino |
| 35 | 29 | 96.7 | 172 | 2 | D90885 | probable resistanc |
| 36 | 29 | 96.7 | 172 | 2 | C85733 | probable resistanc |
| 37 | 29 | 96.7 | 207 | 2 | AI2505 | hypothetical prote |
| 38 | 29 | 96.7 | 209 | 2 | S70662 | galactose-binding |
| 39 | 29 | 96.7 | 223 | 2 | AG1166 | Ribulose-5-Phospha |
| 40 | 29 | 96.7 | 248 | 2 | C83865 | hypothetical prote |
| 41 | 29 | 96.7 | 276 | 2 | D84021 | hypothetical prote |
| 42 | 29 | 96.7 | 278 | 2 | A49505 | lectin light chain |
| 43 | 29 | 96.7 | 288 | 2 | A48452 | galactose-inhibita |
| 44 | 29 | 96.7 | 288 | 2 | B90043 | conserved hypothet |
| 45 | 29 | 96.7 | 298 | 2 | G72522 | hypothetical prote |

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 30; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 3 VYIHP 7

RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 30; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 3 VYIHP 7

RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 30; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 3 VYIHP 7

RESULT 4
C71329
hypothetical protein TP0404 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: C71329
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: C71329
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-177 <COL>
A;Cross-references: GB:AE001218; GB:AE000520; NID:g3322678; PIDN:AAC65395.1; PID:g332269
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0404

Query Match 100.0%; Score 30; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 3 VYIHP 7

RESULT 5
AC1584
hypothetical protein lin1212 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AC1584
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1584
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96443.1; PID:g16413686; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1212

Query Match 100.0%; Score 30; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 92 VYIHP 96

RESULT 6
T50372
probable ATP-dependent RNA helicase cdc28 [imported] - fission yeast (Schizosaccharom
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 15-Sep-2000 #text_change 17-Nov-2000
C;Accession: T50372; T39792
R;Skelton, J.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A;Reference number: Z25066
A;Accession: T50372
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-262 <SKE>
A;Cross-references: EMBL:AL135748; PIDN:CAB63784.1; GSPDB:GN00067; SPDB:SPBC874.01
A;Experimental source: strain 972h(-); cosmid c874
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39792
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 229-349 <MCD>
A;Cross-references: EMBL:AL109731; PIDN:CAB52028.1; GSPDB:GN00067; SPDB:SPBC19C2.01
C;Genetics:
A;Gene: SPBC19C2.01; SPDB:SPBC874.01
A;Map position: 2

Query Match 100.0%; Score 30; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 284 VYIHP 288

RESULT 7
G84459
probable GDP-mannose pyrophosphorylase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84459
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: G84459
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-385 <STO>
A;Cross-references: GB:AE002093; NID:g4544432; PIDN:AAD22341.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g04650
A;Map position: 2

Query Match 100.0%; Score 30; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
||||| 
Db 292 VYIHP 296

RESULT 8
G96778
hypothetical protein F9E10.24 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96778
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: G96778
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-415 <STO>
A;Cross-references: GB:AE005173; NID:g6646773; PIDN:AAF21085.1; GSPDB:GN00141
C;Genetics:
A;Gene: F9E10.24
A;Map position: 1

Query Match 100.0%; Score 30; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
||||| 
Db 301 VYIHP 305

RESULT 9
A49125
gastrulation regulatory protein Zf-T - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49125
R;Schulte-Merker, S.; Ho, R.K.; Herrmann, B.G.; Nusslein-Volhard, C.
Development 116, 1021-1032, 1992
A;Title: The protein product of the zebrafish homologue of the mouse T gene is expressed
A;Reference number: A49125; MUID:93201989
A;Accession: A49125
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <SCH>
A;Cross-references: GB:S57147; NID:g299316; PIDN:AAB25829.1; PID:g299317
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:127982, NCBIP:127985)
C;Superfamily: mouse gene T protein; T-box homology
F;44-220/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
||||| 
Db 116 VYIHP 120

RESULT 10
A41056
brachyury homolog - African clawed frog
N;Alternate names: gene T homolog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A41056
R;Smith, J.C.; Price, B.M.J.; Green, J.B.A.; Weigel, D.; Herrmann, B.G.
Cell 67, 79-87, 1991
A;Title: Expression of a Xenopus homolog of Brachyury (T) is an immediate-early respo
A;Reference number: A41056; MUID:92005698
A;Accession: A41056
A;Molecule type: mRNA
A;Residues: 1-432 <SMI>
A;Cross-references: GB:M77243; NID:g213999; PIDN:AAA49663.1; PID:g214000
C;Comment: Both basic fibroblast growth factor (bFGF) and activin A induce expression
C;Genetics:
A;Gene: Xbra
C;Superfamily: mouse gene T protein; T-box homology
C;Keywords: DNA binding; mesoderm; transcription regulation
F;49-225/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
||||| 
Db 121 VYIHP 125

RESULT 11
S08156
gene T protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S08156
R;Herrmann, B.G.; Labeit, S.; Poustka, A.; King, T.R.; Lehrach, H.
Nature 343, 617-622, 1990
A;Title: Cloning of the T gene required in mesoderm formation in the mouse.
A;Reference number: S08156; MUID:90158787
A;Accession: S08156
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-436 <HER>
A;Cross-references: GB:X51683; NID:g55053; PIDN:CAA35985.1; PID:g55054
C;Genetics:
A;Gene: T
A;Map position: 17
C;Superfamily: mouse gene T protein; T-box homology
C;Keywords: DNA binding; transcription regulation
F;51-227/Domain: T-box homology <TBX>

Query Match 100.0%; Score 30; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
||||| 
Db 123 VYIHP 127

```
RESULT 12
T20803
hypothetical protein F12F6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20803
R;Kershaw, J.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19326
A;Accession: T20803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z73425; PIDN:CAA97789.1; GSPDB:GN00022; CESP:F12F6.3
A;Experimental source: clone F12F6
C;Genetics:
A;Gene: CESP:F12F6.3
A;Map position: 4
A;Introns: 27/2; 75/2; 101/2; 161/3; 188/3; 243/3; 284/2; 388/3; 428/3


  Query Match             100.0%;  Score 30;  DB 2;  Length 444;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     47 VYIHP 51


RESULT 13
JC2318
angiotensin precursor - sheep
N;Alternate names: angiotensinogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC2318; A25406
R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
A;Reference number: JC2318; MUID:95072318
A;Accession: JC2318
A;Molecule type: mRNA
A;Residues: 1-476 <NAG>
A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 465 as Leu
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A;Title: Purification and characterization of ovine angiotensinogen.
A;Reference number: A25406; MUID:86136099
A;Accession: A25406
A;Molecule type: protein
A;Residues: 25-37,'X',39 <FER>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-476/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin #status predicted <MAT>
F;295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 30;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     27 VYIHP 31


RESULT 14
ANRT
```

```
angiotensin precursor - rat
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849
A;Accession: A93945
A;Molecule type: mRNA
A;Residues: 1-477 <OHK>
A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, char
A;Reference number: A90456; MUID:82091819
A;Accession: A90456
A;Molecule type: protein
A;Residues: 25-41 <BOU>
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin I #status experimental <PP1>
F;25-32/Product: angiotensin II #status experimental <PP2>
F;26-32/Product: angiotensin III #status experimental <PP3>
F;295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 30;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     27 VYIHP 31


RESULT 15
A29978
angiotensin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29978
R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A;Title: Molecular cloning of the mouse angiotensinogen gene.
A;Reference number: A29978; MUID:88284703
A;Accession: A29978
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-477 <CLO>
A;Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427
C;Genetics:
A;Introns: 277/1; 366/2; 414/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MAT>


  Query Match             100.0%;  Score 30;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
```

```
          |||||
Db      27 VYIHP 31
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Search completed: July 1, 2002, 07:46:29
Job time: 450 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:07 ; Search time 34.05 Seconds
(without alignments)
5.686 Million cell updates/sec

Title: US-09-723-197-6
Perfect score: 30
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 30 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 30 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 3 | 30 | 100.0 | 177 | 1 | Y404_TREPA | O83419 treponema p |
| 4 | 30 | 100.0 | 378 | 1 | EXT1_CAEEL | O01704 caenorhabdi |
| 5 | 30 | 100.0 | 397 | 1 | TBXT_CHICK | P79778 gallus gall |
| 6 | 30 | 100.0 | 423 | 1 | BRAC_BRARE | Q07998 brachydanio |
| 7 | 30 | 100.0 | 432 | 1 | BRAC_XENLA | P24781 xenopus lae |
| 8 | 30 | 100.0 | 433 | 1 | BRAC_CHICK | P79777 gallus gall |
| 9 | 30 | 100.0 | 435 | 1 | BRAC_HUMAN | O15178 homo sapien |
| 10 | 30 | 100.0 | 436 | 1 | BRAC_MOUSE | P20293 mus musculu |
| 11 | 30 | 100.0 | 436 | 1 | TBX6_HUMAN | O95947 homo sapien |
| 12 | 30 | 100.0 | 440 | 1 | BRA2_BRAFL | P80492 branchiosto |
| 13 | 30 | 100.0 | 448 | 1 | BRA1_BRAFL | Q17134 branchiosto |
| 14 | 30 | 100.0 | 448 | 1 | TX19_HUMAN | O60806 homo sapien |
| 15 | 30 | 100.0 | 476 | 1 | ANGT_SHEEP | P20757 ovis aries |
| 16 | 30 | 100.0 | 477 | 1 | ANGT_MOUSE | P11859 mus musculu |
| 17 | 30 | 100.0 | 477 | 1 | ANGT_RAT | P01015 rattus norv |
| 18 | 30 | 100.0 | 485 | 1 | ANGT_HUMAN | P01019 homo sapien |
| 19 | 30 | 100.0 | 501 | 1 | TX18_HUMAN | O95935 homo sapien |
| 20 | 30 | 100.0 | 540 | 1 | TBX6_MOUSE | P70327 mus musculu |
| 21 | 30 | 100.0 | 602 | 1 | TX15_MOUSE | O70306 mus musculu |
| 22 | 30 | 100.0 | 613 | 1 | TX18_MOUSE | Q9epz6 mus musculu |
| 23 | 30 | 100.0 | 678 | 1 | SIR1_YEAST | P21691 saccharomyc |
| 24 | 30 | 100.0 | 980 | 1 | SYV_SCHPO | O75005 schizosacch |
| 25 | 30 | 100.0 | 1055 | 1 | CC28_SCHPO | Q10752 schizosacch |
| 26 | 30 | 100.0 | 1121 | 1 | DDX8_ARATH | Q38953 arabidopsis |
| 27 | 30 | 100.0 | 1200 | 1 | DDX8_CAEEL | Q09530 caenorhabdi |
| 28 | 30 | 100.0 | 1220 | 1 | DDX8_HUMAN | Q14562 homo sapien |
| 29 | 30 | 100.0 | 1267 | 1 | DHR1_YEAST | Q04217 saccharomyc |
| 30 | 30 | 100.0 | 1355 | 1 | VG46_HSVI1 | Q00104 ictalurid h |
| 31 | 29 | 96.7 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 32 | 29 | 96.7 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 33 | 29 | 96.7 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 34 | 29 | 96.7 | 172 | 1 | YNCA_ECOLI | P76112 escherichia |
| 35 | 29 | 96.7 | 288 | 1 | GIL2_ENTHI | Q03077 entamoeba h |
| 36 | 29 | 96.7 | 391 | 1 | PYRC_USTMA | P31301 ustilago ma |
| 37 | 29 | 96.7 | 471 | 1 | BRAC_HALRO | P56158 halocynthia |
| 38 | 29 | 96.7 | 528 | 1 | GD_DROME | O62589 drosophila |
| 39 | 29 | 96.7 | 617 | 1 | THRB_RAT | P18292 rattus norv |
| 40 | 29 | 96.7 | 622 | 1 | THRB_HUMAN | P00734 homo sapien |
| 41 | 29 | 96.7 | 625 | 1 | THRB_BOVIN | P00735 bos taurus |
| 42 | 29 | 96.7 | 692 | 1 | EOMD_XENLA | P79944 xenopus lae |
| 43 | 29 | 96.7 | 702 | 1 | CRN_DROME | P17886 drosophila |
| 44 | 28 | 93.3 | 11 | 1 | ANGT_CRIGE | P09037 crinia geor |
| 45 | 28 | 93.3 | 144 | 1 | SALT_ORYSA | P24120 oryza sativ |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 30; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5
|||||
Db 3 VYIHP 7

RESULT 2
ANGT_HORSE
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";

```
RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      3 VYIHP 7


RESULT   3
Y404_TREPA
ID   Y404_TREPA     STANDARD;      PRT;   177 AA.
AC   O83419;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein TP0404.
GN   TP0404.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NICHOLS;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001218; AAC65395.1; -.
DR   TIGR; TP0404; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   177 AA;  19491 MW;  A9395B74FA052F93 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 177;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db      3 VYIHP 7


RESULT   4
EXT1_CAEEL
ID   EXT1_CAEEL     STANDARD;      PRT;   378 AA.
AC   O01704;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Multiple exostoses homolog 1.
GN   RIB-1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97264342; PubMed=9110175;
RA   Clines G.A., Ashley J.A., Shah S., Lovett M.;
RT   "The structure of the human multiple exostoses 2 gene and
RT   characterization of homologs in mouse and Caenorhabditis elegans.";
RL   Genome Res. 7:359-367(1997).
CC   -!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U94834; AAC47509.1; -.
SQ   SEQUENCE   378 AA;  44453 MW;  5CE6ECF3AA89647E CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 378;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     43 VYIHP 47


RESULT   5
TBXT_CHICK
ID   TBXT_CHICK     STANDARD;      PRT;   397 AA.
AC   P79778;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box containing protein TBXT.
GN   TBXT.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WHITE LEGHORN; TISSUE=Embryo;
RX   MEDLINE=97178976; PubMed=9053317;
RA   Knezevic V., de Santo R., Mackem S.;
RT   "Two novel chick T-box genes related to mouse Brachyury are expressed
RT   in different, non-overlapping mesodermal domains during
RT   gastrulation.";
RL   Development 124:411-419(1997).
CC   -!- FUNCTION: MAY BE INVOLVED IN THE INITIAL FORMATION OF THE
CC       CHORDAMESODERM.
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CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN THE EARLY PRIMITIVE
CC       STREAK. BY STAGE 4, IN HENSEN'S NODE, EARLY PRECHORDAL PLATE AND
CC       NOTOCHORD. ALSO EXPRESSED IN EARLY DEVELOPMENT IN THE NEURAL
CC       PLATE ECTODERM IMMEDIATELY ANTERIOR TO HENSEN'S NODE. EXPRESSION
CC       NOT DETECTED AFTER STAGE 10-12.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U67087; AAC60072.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein.
FT   DNA_BIND     48    216       T-BOX.
SQ   SEQUENCE   397 AA;  43686 MW;  8F137C7D271D393B CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    120 VYIHP 124


RESULT   6
BRAC_BRARE
ID   BRAC_BRARE     STANDARD;      PRT;   423 AA.
AC   Q07998;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein homolog (T protein homolog) (T-box protein ZFT) (ZF-
DE   T).
GN   T OR NTL.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=93201989; PubMed=1295726;
RA   Schulte-Merker S., Ho R.K., Herrmann B.G., Nuesslein-Volhard C.;
RT   "The protein product of the zebrafish homologue of the mouse T gene
RT   is expressed in nuclei of the germ ring and the notochord of the
RT   early embryo.";
RL   Development 116:1021-1032(1992).
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM DIFFERENTIATION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: EARLY EMBRYO. HIGHEST LEVELS FOUND AT ALL
CC       STAGES IN DEVELOPING NOTOCHORD. ALSO FOUND, BEFORE GASTRULATION,
CC       IN THE PRESUMPTIVE MESODERM AND ENDODERM (THE GERM RING) AS WELL
CC       AS IN ENVELOPING CELLS.
CC   -!- DEVELOPMENTAL STAGE: IN DEVELOPING EMBRYO, FIRST EXPRESSED IN THE
CC       DOMING STAGE (4.2 HOURS). HIGHEST EXPRESSION FOUND BETWEEN 5.2 AND
CC       9.5 HOURS (EPIBOLY) AFTER WHICH, LEVELS GRADUALLY DECREASE AND BY
CC       48 HOURS, NO MORE EXPRESSION IS OBSERVED.
CC   -!- INDUCTION: BY MESODERM-INDUCING FACTOR ACTIVIN A.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S57147; AAB25829.1; -.
DR   HSSP; P24781; 1XBR.
DR   ZFIN; ZDB-GENE-980526-437; ntl.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Activator.
FT   DNA_BIND     44    212       T-BOX.
SQ   SEQUENCE   423 AA;  45834 MW;  96FEB8109EF4407E CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    116 VYIHP 120


RESULT   7
BRAC_XENLA
ID   BRAC_XENLA     STANDARD;      PRT;   432 AA.
AC   P24781;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein (T protein) (XBRA).
GN   BRA.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92005698; PubMed=1717160;
RA   Smith J.C., Price B.M., Green J.B., Weigel D., Herrmann B.G.;
RT   "Expression of a Xenopus homolog of Brachyury (T) is an immediate-
RT   early response to mesoderm induction.";
RL   Cell 67:79-87(1991).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=94147980; PubMed=7906224;
RA   Cunliffe V., Smith J.C.;
RT   "Specification of mesodermal pattern in Xenopus laevis by
RT   interactions between Brachyury, noggin and Xwnt-8.";
RL   EMBO J. 13:349-359(1994).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 39-222.
RX   MEDLINE=98007980; PubMed=9349824;
RA   Mueller C.W., Herrmann B.G.;
RT   "Crystallographic structure of the T domain-DNA complex of the
RT   Brachyury transcription factor.";
RL   Nature 389:884-888(1997).
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CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. CAUSES DORSAL
CC       MESODERMAL DIFFERENTIATION OF ANIMAL CAP ECTODERM WHEN CO-
CC       EXPRESSED WITH XWNT-8 AND NOGGIN. NONE OF THESE MOLECULES CAUSES
CC       DORSAL MESODERM FORMATION WHEN EXPRESSED ALONE.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN PRESUMPTIVE MESODERMAL CELLS
CC       AROUND THE BLASTOPORE, AND THEN IN THE NOTOCHORD.
CC   -!- DEVELOPMENTAL STAGE: DURING GASTRULA AND NEURULA STAGES IN
CC       INVOLUTING MESODERM AND IN THE NOTOCHORD.
CC   -!- INDUCTION: BY THE NATURAL SIGNAL AND IN RESPONSE TO THE MESODERM-
CC       INDUCING FACTORS ACTIVIN A AND BASIC FGF.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M77243; AAA49663.1; -.
DR   PIR; A41056; A41056.
DR   PDB; 1XBR; 14-JAN-98.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Activator; 3D-structure.
FT   DNA_BIND     49    217       T-BOX.
SQ   SEQUENCE   432 AA;  47599 MW;  2F91D942D86EE60A CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    121 VYIHP 125


RESULT   8
BRAC_CHICK
ID   BRAC_CHICK     STANDARD;      PRT;   433 AA.
AC   P79777; Q90654;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein (T protein).
GN   T.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=95246917; PubMed=7729577;
RA   Kispert A., Ortner H., Cooke J., Herrmann B.G.;
RT   "The chick Brachyury gene: developmental expression pattern and
RT   response to axial induction by localized activin.";
RL   Dev. Biol. 168:406-415(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WHITE LEGHORN; TISSUE=Embryo;
RX   MEDLINE=97178976; PubMed=9053317;
RA   Knezevic V., de Santo R., Mackem S.;
RT   "Two novel chick T-box genes related to mouse Brachyury are expressed
RT   in different, non-overlapping mesodermal domains during
RT   gastrulation.";
RL   Development 124:411-419(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Huang J.X., Wendler C.C., Morrice D.R., Burt D.W., Runyan R.B.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A
CC       PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION
CC       WHEN BOUND TO SUCH A SITE (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN THE POSTERIOR EPIBLAST OF
CC       STAGE XIII BLASTODERM, THEN IN THE ELONGATING PRIMITIVE STREAK,
CC       EARLY MIGRATING MESODERM, HENSEN'S NODE AND IN THE NOTOCHORD.
CC       IN LATER STAGES, FOUND IN TAIL BUD AND ENTIRE NOTOCHORD UP TO
CC       STAGE 26-28.
CC   -!- INDUCTION: BY FGF-4 AND ACTIVIN.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67086; AAC60283.1; -.
DR   EMBL; U25176; AAA67365.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Activator.
FT   DNA_BIND     49    217       T-BOX.
FT   CONFLICT    250    250       A -> T (IN REF. 3).
SQ   SEQUENCE   433 AA;  47289 MW;  8C0C27577E82872F CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    121 VYIHP 125


RESULT   9
BRAC_HUMAN
ID   BRAC_HUMAN     STANDARD;      PRT;   435 AA.
AC   O15178;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein (T protein).
GN   T.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=96402060; PubMed=8963900;
RA   Edwards Y.H., Putt W., Lekoape K.M., Stott D., Fox M., Hopkinson D.A.,
RA   Sowden J.;
RT   "The human homolog T of the mouse T(Brachyury) gene; gene structure,
RT   cDNA sequence, and assignment to chromosome 6q27.";
RL   Genome Res. 6:226-233(1996).
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A
CC       PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION
CC       WHEN BOUND TO SUCH A SITE.
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AJ001699; CAA04938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 601397; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Activator.
FT   DNA_BIND     51    219       T-BOX.
SQ   SEQUENCE   435 AA;  47443 MW;  9D470088C8602631 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    123 VYIHP 127


RESULT  10
BRAC_MOUSE
ID   BRAC_MOUSE     STANDARD;      PRT;   436 AA.
AC   P20293;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein (T protein).
GN   T.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90158787; PubMed=2154694;
RA   Herrmann B.G., Labeit S., Poustka A., King T.R., Lehrach H.;
RT   "Cloning of the T gene required in mesoderm formation in the mouse.";
RL   Nature 343:617-622(1990).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=93345466; PubMed=8344258;
RA   Kispert A., Herrmann B.G.;
RT   "The Brachyury gene encodes a novel DNA binding protein.";
RL   EMBO J. 12:3211-3220(1993).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=96030782; PubMed=7588606;
RA   Kispert A., Koschorz B., Herrmann B.G.;
RT   "The T protein encoded by Brachyury is a tissue-specific
RT   transcription factor.";
RL   EMBO J. 14:4763-4772(1995).
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION. BINDS TO A
CC       PALINDROMIC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION
CC       WHEN BOUND TO SUCH A SITE.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- DEVELOPMENTAL STAGE: DURING GASTRULA AND NEURULA STAGES IN
CC       INVOLUTING MESODERM AND IN THE NOTOCHORD.
CC   -!- DISEASE: EMBRYO LACKING THE T GENE FAIL TO FORM THE NOTOCHORD,
CC       THE ENTIRE POSTERIOR REGION AND THE ALLANTOIS, AND DIE AT ABOUT
CC       10 DAYS OF GESTATION.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X51683; CAA35985.1; -.
DR   PIR; S08156; S08156.
DR   HSSP; P24781; 1XBR.
DR   TRANSFAC; T01526; -.
DR   MGD; MGI:98472; T.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Activator.
FT   DNA_BIND     51    219       T-BOX.
SQ   SEQUENCE   436 AA;  47440 MW;  1A0BDF9BA7FC2484 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    123 VYIHP 127


RESULT  11
TBX6_HUMAN
ID   TBX6_HUMAN     STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
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RN   [2]
RP   SEQUENCE OF 135-272 FROM N.A.
RC   TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    172 VYIHP 176


RESULT  12
BRA2_BRAFL
ID   BRA2_BRAFL     STANDARD;      PRT;   440 AA.
AC   P80492;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein homolog 2 (AmBra-2).
GN   BRA-2.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96125169; PubMed=8575328;
RA   Holland P.W.H., Koschorz B., Holland L.Z., Herrmann B.G.;
RT   "Conservation of Brachyury (T) genes in amphioxus and vertebrates:
RT   developmental and evolutionary implications.";
RL   Development 121:4283-4291(1995).
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: MESODERM AND NOTOCHORD.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Multigene family.
FT   DNA_BIND     44    215       T-BOX.
SQ   SEQUENCE   440 AA;  48469 MW;  F12EBC417243D3D6 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 440;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    116 VYIHP 120


RESULT  13
BRA1_BRAFL
ID   BRA1_BRAFL     STANDARD;      PRT;   448 AA.
AC   Q17134;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Brachyury protein homolog 1 (AmBra-1).
GN   BRA-1.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Larva;
RX   MEDLINE=96125169; PubMed=8575328;
RA   Holland P.W.H., Koschorz B., Holland L.Z., Herrmann B.G.;
RT   "Conservation of Brachyury (T) genes in amphioxus and vertebrates:
RT   developmental and evolutionary implications.";
RL   Development 121:4283-4291(1995).
CC   -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES
CC       REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE 10 H GASTRULA AROUND
CC       THE BLASTOPORE. IN LATER STAGES OF GASTRULATION AND EARLY
CC       NEURALIZATION, EXPRESSED IN POSTERIOR MESODERM AND THE NOTOCHORD
CC       WHERE EXPRESSION CONTINUES AT LEAST UNTIL SWIMMING LARVAL STAGE.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X91903; CAA62999.1; -.
DR   HSSP; P24781; 1XBR.
```

```
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Developmental protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Multigene family.
FT   DNA_BIND     54    224       T-BOX.
SQ   SEQUENCE   448 AA;  49253 MW;  43326D32FD4BC156 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 448;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    126 VYIHP 130


RESULT  14
TX19_HUMAN
ID   TX19_HUMAN     STANDARD;      PRT;   448 AA.
AC   O60806;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX19 (T-box protein 19).
GN   TBX19.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
RN   [2]
RP   SEQUENCE OF 3-437 FROM N.A.
RA   Wray P.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ010277; CAB37936.1; -.
DR   EMBL; AL009051; CAA15624.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 604614; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DNA_BIND     50    218       T-BOX.
SQ   SEQUENCE   448 AA;  48238 MW;  B7B1DFF14B8B53C5 CRC64;


  Query Match             100.0%;  Score 30;  DB 1;  Length 448;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    122 VYIHP 126


RESULT  15
ANGT_SHEEP
ID   ANGT_SHEEP     STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL       1     24
FT   CHAIN       25    476       ANGIOTENSINOGEN.
FT   PEPTIDE     25     34       ANGIOTENSIN I.
FT   PEPTIDE     25     32       ANGIOTENSIN II.
FT   CARBOHYD   295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;
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Query Match 100.0%; Score 30; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 VYIHP 5
           |||||
Db      27 VYIHP 31
```

Search completed: July 1, 2002, 07:47:08
Job time: 474 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:11 ; Search time 122.73 Seconds
(without alignments)
7.048 Million cell updates/sec

Title: US-09-723-197-6
Perfect score: 30
Sequence: 1 VYIHP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 30 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 2 | 30 | 100.0 | 63 | 6 | Q95KV3 | Q95kv3 bos taurus |
| 3 | 30 | 100.0 | 101 | 12 | Q9EN21 | Q9en21 amsacta moo |
| 4 | 30 | 100.0 | 124 | 16 | Q98AY8 | Q98ay8 rhizobium l |
| 5 | 30 | 100.0 | 130 | 13 | P79705 | P79705 cynops pyrr |
| 6 | 30 | 100.0 | 171 | 17 | Q971G2 | Q971g2 sulfolobus |
| 7 | 30 | 100.0 | 183 | 5 | Q9N866 | Q9n866 leishmania |
| 8 | 30 | 100.0 | 184 | 4 | O75406 | O75406 homo sapien |
| 9 | 30 | 100.0 | 184 | 16 | Q92CG0 | Q92cg0 listeria in |
| 10 | 30 | 100.0 | 245 | 6 | Q95J13 | Q95j13 pan troglod |
| 11 | 30 | 100.0 | 265 | 5 | Q9XYF5 | Q9xyf5 hydra atten |
| 12 | 30 | 100.0 | 295 | 4 | Q9HA44 | Q9ha44 homo sapien |
| 13 | 30 | 100.0 | 295 | 5 | O96040 | O96040 ptychodera |
| 14 | 30 | 100.0 | 317 | 11 | Q923Q5 | Q923q5 mus musculu |
| 15 | 30 | 100.0 | 323 | 5 | Q9VZ11 | Q9vz11 drosophila |
| 16 | 30 | 100.0 | 344 | 13 | Q98SM4 | Q98sm4 eleutheroda |
| 17 | 30 | 100.0 | 382 | 5 | Q9U3J6 | Q9u3j6 caenorhabdi |
| 18 | 30 | 100.0 | 385 | 10 | Q9SJ94 | Q9sj94 arabidopsis |
| 19 | 30 | 100.0 | 399 | 4 | Q9Y5P5 | Q9y5p5 homo sapien |
| 20 | 30 | 100.0 | 402 | 5 | Q95WL2 | Q95wl2 hydractinia |
| 21 | 30 | 100.0 | 411 | 10 | Q9SSG7 | Q9ssg7 arabidopsis |
| 22 | 30 | 100.0 | 415 | 10 | Q9C9P3 | Q9c9p3 arabidopsis |
| 23 | 30 | 100.0 | 418 | 13 | Q90ZA4 | Q90za4 ambystoma m |
| 24 | 30 | 100.0 | 419 | 10 | Q9FQ10 | Q9fq10 medicago tr |
| 25 | 30 | 100.0 | 419 | 13 | O42100 | O42100 oryzias lat |
| 26 | 30 | 100.0 | 420 | 4 | Q9NWC3 | Q9nwc3 homo sapien |
| 27 | 30 | 100.0 | 420 | 4 | Q96IJ6 | Q96ij6 homo sapien |
| 28 | 30 | 100.0 | 420 | 11 | Q922H4 | Q922h4 mus musculu |
| 29 | 30 | 100.0 | 434 | 13 | Q9W7R8 | Q9w7r8 xenopus lae |
| 30 | 30 | 100.0 | 435 | 6 | Q9GL27 | Q9gl27 canis famil |
| 31 | 30 | 100.0 | 436 | 11 | Q9CSJ0 | Q9csj0 mus musculu |
| 32 | 30 | 100.0 | 439 | 13 | O57386 | O57386 cynops pyrr |
| 33 | 30 | 100.0 | 442 | 5 | Q9GNV1 | Q9gnv1 platynereis |
| 34 | 30 | 100.0 | 446 | 11 | Q99ME7 | Q99me7 mus musculu |
| 35 | 30 | 100.0 | 449 | 4 | Q9BVA6 | Q9bva6 homo sapien |
| 36 | 30 | 100.0 | 461 | 11 | Q9D2V0 | Q9d2v0 mus musculu |
| 37 | 30 | 100.0 | 477 | 4 | Q96FD5 | Q96fd5 homo sapien |
| 38 | 30 | 100.0 | 485 | 4 | Q96F91 | Q96f91 homo sapien |
| 39 | 30 | 100.0 | 485 | 6 | Q9GLP7 | Q9glp7 pan troglod |
| 40 | 30 | 100.0 | 485 | 6 | Q9GLP6 | Q9glp6 gorilla gor |
| 41 | 30 | 100.0 | 485 | 6 | Q9GLN8 | Q9gln8 pan troglod |
| 42 | 30 | 100.0 | 486 | 6 | Q9TSZ0 | Q9tsz0 callithrix |
| 43 | 30 | 100.0 | 513 | 10 | Q9LWF6 | Q9lwf6 oryza sativ |
| 44 | 30 | 100.0 | 533 | 4 | Q96SF7 | Q96sf7 homo sapien |
| 45 | 30 | 100.0 | 695 | 5 | Q9XUQ0 | Q9xuq0 caenorhabdi |

ALIGNMENTS

RESULT 1
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYIHP 5

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          |||||
Db      3 VYIHP 7


RESULT   2
Q95KV3
ID   Q95KV3      PRELIMINARY;      PRT;    63 AA.
AC   Q95KV3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BRACHYURY PROTEIN (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   de Wit A.A.C., Boerjan M.L., Kruip T.A.M.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ413216; CAC88365.1; -.
FT   NON_TER       1      1
FT   NON_TER      63     63
SQ   SEQUENCE   63 AA;  7130 MW;  67B9163720413171 CRC64;


  Query Match             100.0%;  Score 30;  DB 6;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VYIHP 5
          |||||
Db      58 VYIHP 62


RESULT   3
Q9EN21
ID   Q9EN21      PRELIMINARY;      PRT;   101 AA.
AC   Q9EN21;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AMV027.
GN   AMV027.
OS   Amsacta moorei entomopoxvirus (AmEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC   Entomopoxvirus B.
OX   NCBI_TaxID=28321;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20396580; PubMed=10936094;
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RT   "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT   Analysis and Comparison with Other Poxviruses.";
RL   Virology 274:120-139(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF250284; AAG02733.1; -.
SQ   SEQUENCE   101 AA;  12286 MW;  7ECA507CD63762CC CRC64;


  Query Match             100.0%;  Score 30;  DB 12;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VYIHP 5
          |||||
Db      76 VYIHP 80
```

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RESULT   4
Q98AY8
ID   Q98AY8      PRELIMINARY;      PRT;   124 AA.
AC   Q98AY8;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   MLL5800 PROTEIN.
GN   MLL5800.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP003007; BAB52184.1; -.
KW   Complete proteome.
SQ   SEQUENCE   124 AA;  13781 MW;  F1280829A42DD9A2 CRC64;


  Query Match             100.0%;  Score 30;  DB 16;  Length 124;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 VYIHP 5
          |||||
Db      51 VYIHP 55


RESULT   5
P79705
ID   P79705      PRELIMINARY;      PRT;   130 AA.
AC   P79705;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   BRACHURY (FRAGMENT).
OS   Cynops pyrrhogaster (Japanese common newt).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX   NCBI_TaxID=8330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYO;
RA   Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takeshima K.,
RA   Kaneda T.;
RT   "Serial expression of the genes in a mesodermalizing ectoderms of
RT   early Cynops gastrula.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D89442; BAA13957.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14671 MW;  B1A834C01890D025 CRC64;
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  Query Match             100.0%;  Score 30;  DB 13;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     61 VYIHP 65


RESULT   6
Q971G2
ID   Q971G2      PRELIMINARY;      PRT;   171 AA.
AC   Q971G2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN ST1391.
GN   ST1391.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000986; BAB66458.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   171 AA;  18700 MW;  897F397EAD34EF0A CRC64;


  Query Match             100.0%;  Score 30;  DB 17;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     18 VYIHP 22


RESULT   7
Q9N866
ID   Q9N866      PRELIMINARY;      PRT;   183 AA.
AC   Q9N866;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE.
GN   L8382.11.
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FRIEDLIN;
RA   Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL365476; CAB97039.1; -.
KW   Helicase.
SQ   SEQUENCE   183 AA;  20551 MW;  BEE0ED6545831F85 CRC64;


  Query Match             100.0%;  Score 30;  DB 5;  Length 183;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    129 VYIHP 133


RESULT   8
O75406
ID   O75406      PRELIMINARY;      PRT;   184 AA.
AC   O75406;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HUNTINGTIN INTERACTING PROTEIN HYPE (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FRONTAL CORTEX;
RA   Faber P.W., Barnes G.T., Srinidhi J., Chen J., Gusella J.F.,
RA   MacDonald M.E.;
RT   "Huntingtin interacts with a family of WW domain proteins.";
RL   Hum. Mol. Genet. 0:0-0(1998).
DR   EMBL; AF049611; AAC26847.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   184 AA;  20919 MW;  5FB5DE1093D99B20 CRC64;


  Query Match             100.0%;  Score 30;  DB 4;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     86 VYIHP 90


RESULT   9
Q92CG0
ID   Q92CG0      PRELIMINARY;      PRT;   184 AA.
AC   Q92CG0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LIN1212 PROTEIN.
GN   LIN1212.
OS   Listeria innocua.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Listeria.
OX   NCBI_TaxID=1642;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIP 11262 / SEROVAR 6A;
RX   PubMed=11679669;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
DR   EMBL; AL596168; CAC96443.1; -.
DR   ListiList; LIN01212; -.
KW   Complete proteome.
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SQ   SEQUENCE   184 AA;  21570 MW;  5A842734193A7F66 CRC64;


  Query Match            100.0%;  Score 30;  DB 16;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     92 VYIHP 96


RESULT  10
Q95J13
ID   Q95J13      PRELIMINARY;      PRT;   245 AA.
AC   Q95J13;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
GN   REN.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=504, AND 505;
RA   Satta Y.;
RT   "Comparison of DNA and protein polymorphims between humans and
RT   chimpanzees.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062027; BAB55856.1; -.
DR   EMBL; AB062028; BAB55857.1; -.
FT   NON_TER     245    245
SQ   SEQUENCE   245 AA;  26317 MW;  E0092390B9803E0B CRC64;


  Query Match            100.0%;  Score 30;  DB 6;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     36 VYIHP 40


RESULT  11
Q9XYF5
ID   Q9XYF5      PRELIMINARY;      PRT;   265 AA.
AC   Q9XYF5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   BRACHYURY HOMOLOG HYBRA1 (FRAGMENT).
GN   HYBRA1.
OS   Hydra attenuata (Hydra) (Hydra vulgaris).
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydridae; Hydra.
OX   NCBI_TaxID=6087;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZURICH;
RX   MEDLINE=99128189; PubMed=9927600;
RA   Technau U., Bode H.R.;
RT   "HyBra1, a Brachyury homologue, acts during head formation in Hydra.";
RL   Development 126:999-1010(1999).
DR   EMBL; AF105065; AAD26626.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
FT   NON_TER     265    265
SQ   SEQUENCE   265 AA;  30288 MW;  C61B6B5EAAF33545 CRC64;


  Query Match            100.0%;  Score 30;  DB 5;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    118 VYIHP 122


RESULT  12
Q9HA44
ID   Q9HA44      PRELIMINARY;      PRT;   295 AA.
AC   Q9HA44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE   TRANSCRIPTION FACTOR TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022330; BAB14014.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33197 MW;  F2BD3E53E0ED21E0 CRC64;


  Query Match            100.0%;  Score 30;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    172 VYIHP 176


RESULT  13
O96040
ID   O96040      PRELIMINARY;      PRT;   295 AA.
AC   O96040;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PFBRA1.
OS   Ptychodera flava.
OC   Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;
OC   Ptychodera.
OX   NCBI_TaxID=63121;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98413048; PubMed=9739128;
RA   Tagawa K., Humphreys T., Satoh N.;
RT   "Novel pattern of Brachyury gene expression in hemichordate embryos.";
RL   Mech. Dev. 75:139-143(1998).
DR   EMBL; AB004912; BAA37091.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33331 MW;  3438B0D0B4F1EE75 CRC64;


  Query Match             100.0%;  Score 30;  DB 5;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db     96 VYIHP 100


RESULT  14
Q923Q5
ID   Q923Q5      PRELIMINARY;      PRT;   317 AA.
AC   Q923Q5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DM538M10.7 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY)
DE   (OLFACTORY RECEPTOR LIKE) PROTEIN).
GN   DM538M10.7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kay M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136158; CAC43450.1; -.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   317 AA;  34674 MW;  763C856543F7327A CRC64;


  Query Match             100.0%;  Score 30;  DB 11;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    257 VYIHP 261


RESULT  15
Q9VZ11
ID   Q9VZ11      PRELIMINARY;      PRT;   323 AA.
AC   Q9VZ11;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CG12624 PROTEIN.
GN   CG12624.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003485; AAF48020.1; -.
DR   FlyBase; FBgn0030284; CG12624.
DR   InterPro; IPR001320; Ion_glut_receptor.
DR   Pfam; PF00060; lig_chan; 1.
SQ   SEQUENCE   323 AA;  36569 MW;  29948CFA8E818A38 CRC64;


  Query Match             100.0%;  Score 30;  DB 5;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 VYIHP 5
          |||||
Db    168 VYIHP 172


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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds
(without alignments)
4.211 Million cell updates/sec

Title: US-09-723-197-8
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 6 | 17 | AAR95669 | Angiotensin II fra |
| 2 | 34 | 100.0 | 6 | 19 | AAW65604 | Angiotensin II ana |
| 3 | 34 | 100.0 | 6 | 19 | AAW64735 | Angiotensin II pep |
| 4 | 34 | 100.0 | 6 | 19 | AAW71117 | Peptide AII(1-6) u |
| 5 | 34 | 100.0 | 6 | 20 | AAY49593 | Angiotensin analog |
| 6 | 34 | 100.0 | 6 | 20 | AAY33908 | Angiotensin II ana |
| 7 | 34 | 100.0 | 6 | 20 | AAY30546 | Amino acid sequenc |
| 8 | 34 | 100.0 | 6 | 20 | AAY30590 | Amino acid sequenc |
| 9 | 34 | 100.0 | 6 | 20 | AAY32721 | Angiotensin II ana |
| 10 | 34 | 100.0 | 6 | 20 | AAY33775 | Angiotensin II (AI |
| 11 | 34 | 100.0 | 6 | 20 | AAY15352 | Angiotensin II (AI |
| 12 | 34 | 100.0 | 6 | 20 | AAY15312 | Angiotensin II (AI |
| 13 | 34 | 100.0 | 6 | 21 | AAB27408 | Angiotensin II ana |
| 14 | 34 | 100.0 | 6 | 21 | AAB28106 | Angiotensin II ana |
| 15 | 34 | 100.0 | 6 | 21 | AAY84131 | Peptide comprising |
| 16 | 34 | 100.0 | 6 | 21 | AAY77044 | Angiotensin II (AI |
| 17 | 34 | 100.0 | 6 | 21 | AAY57408 | Angiotensin peptid |
| 18 | 34 | 100.0 | 6 | 22 | AAE08878 | AII peptide (resid |
| 19 | 34 | 100.0 | 6 | 22 | AAE02995 | Human angiotensin |
| 20 | 34 | 100.0 | 6 | 22 | AAE03158 | Human angiotensin |
| 21 | 34 | 100.0 | 7 | 17 | AAR95665 | Angiotensin II fra |
| 22 | 34 | 100.0 | 7 | 19 | AAW65600 | Angiotensin II ana |
| 23 | 34 | 100.0 | 7 | 19 | AAW64731 | Angiotensin II pep |
| 24 | 34 | 100.0 | 7 | 19 | AAW71113 | Peptide AII(1-7) u |
| 25 | 34 | 100.0 | 7 | 20 | AAY49589 | Angiotensin analog |
| 26 | 34 | 100.0 | 7 | 20 | AAY50296 | Neutrophil-activat |
| 27 | 34 | 100.0 | 7 | 20 | AAY33904 | Angiotensin II ana |
| 28 | 34 | 100.0 | 7 | 20 | AAY30542 | Amino acid sequenc |
| 29 | 34 | 100.0 | 7 | 20 | AAY30586 | Amino acid sequenc |
| 30 | 34 | 100.0 | 7 | 20 | AAY32717 | Angiotensin II ana |
| 31 | 34 | 100.0 | 7 | 20 | AAY33771 | Angiotensin II (AI |
| 32 | 34 | 100.0 | 7 | 20 | AAY15348 | Angiotensin II (AI |
| 33 | 34 | 100.0 | 7 | 20 | AAY15308 | Angiotensin II (AI |
| 34 | 34 | 100.0 | 7 | 21 | AAB26205 | Anion exchange res |
| 35 | 34 | 100.0 | 7 | 21 | AAB27404 | Angiotensin II ana |
| 36 | 34 | 100.0 | 7 | 21 | AAB28102 | Angiotensin II ana |
| 37 | 34 | 100.0 | 7 | 21 | AAY84565 | Amino acid sequenc |
| 38 | 34 | 100.0 | 7 | 21 | AAY84127 | Peptide comprising |
| 39 | 34 | 100.0 | 7 | 21 | AAY77040 | Angiotensin II (AI |
| 40 | 34 | 100.0 | 7 | 21 | AAY57404 | Angiotensin peptid |
| 41 | 34 | 100.0 | 7 | 22 | AAE08874 | AII peptide (resid |
| 42 | 34 | 100.0 | 7 | 22 | AAE02991 | Human angiotensin |
| 43 | 34 | 100.0 | 7 | 22 | AAE03154 | Human angiotensin |
| 44 | 34 | 100.0 | 7 | 22 | AAB91452 | Angiotensin peptid |
| 45 | 34 | 100.0 | 7 | 22 | AAB91463 | Angiotensin peptid |

ALIGNMENTS

RESULT 1
AAR95669
ID AAR95669 standard; peptide; 6 AA.
XX
AC AAR95669;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(1-6).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 drvyih 6

RESULT 2
AAW65604
ID AAW65604 standard; peptide; 6 AA.
XX
AC AAW65604;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-6).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 drvyih 6

RESULT 3
AAW64735
ID AAW64735 standard; peptide; 6 AA.
XX
AC AAW64735;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #7.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in

CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 drvyih 6

RESULT 4
AAW71117
ID AAW71117 standard; peptide; 6 AA.
XX
AC AAW71117;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-6) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 drvyih 6

RESULT 5
AAY49593
ID AAY49593 standard; peptide; 6 AA.
XX
AC AAY49593;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:8.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIH 6
          ||||||
Db      1 drvyih 6
```

RESULT 6
AAY33908
ID AAY33908 standard; peptide; 6 AA.
XX
AC AAY33908;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-6).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(5-8). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC or AII AT2 type 2 receptor agonists can rapidly provide a large
CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.
CC Similarly, methods that increase in vivo proliferation of ESCs will
CC enhance the utility of replacement therapy by rapidly increasing local
CC concentration of the stem cells and their progeny at the site of
CC therapy. The method also increases the potential utility of ESCs as
CC vehicles for gene therapy in certain disorders by more efficiently
CC providing a large number of such cells for transfection, and also by
CC providing a more efficient means to rapidly expand transfected ESCs.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIH 6
          ||||||
Db      1 drvyih 6
```

RESULT 7

AAY30546
ID AAY30546 standard; peptide; 6 AA.
XX
AC AAY30546;
XX
DT 18-NOV-1999 (first entry)
XX
DE Amino acid sequence of angiotensin II fragment AII1-6.
XX
KW Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS Synthetic.
XX
PN WO9946285-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05261.
XX
PR 11-MAR-1998; 98US-0077499.
PR 12-JUN-1998; 98US-0089064.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551360/46.
XX
PT An improved method for producing a tissue equivalent with angiotensin I
PT and II derived active agents -
XX
PS Claim 2; Page 55; 83pp; English.
XX
CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes an improved method
CC for producing a tissue equivalent. The method comprises contacting
CC the tissue equivalent with angiotensin I and II derived active
CC agents. The methods are used for production and culture of tissue
CC equivalents (three-dimensional cell and tissue culture systems),
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC vascular graft, cartilage, ligament, collagen lattice, liver and
CC kidney tissue equivalents. The methods and tissue culture systems
CC are used for the long-term proliferation of cells and tissues
CC in an in vitro environment that more closely approximates that found
CC in vivo.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||||
Db      1 drvyih 6
```

RESULT 8
AAY30590
ID AAY30590 standard; peptide; 6 AA.
XX
AC AAY30590;
XX
DT 18-NOV-1999 (first entry)
XX
DE Amino acid sequence of an angiotensin II (AII) fragment AII1-6.
XX
KW Angiotensin; analogue; radiation mitigation; tissue damage;
KW radiation therapy; bone marrow transplantation;
KW megakaryocyte production; platelet production; cancer therapy;
KW gene therapy; hematopoietic disorder.

XX
OS Synthetic.
XX
PN WO9945945-A1.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05194.
XX
PR 10-MAR-1998; 98US-0077382.
PR 09-APR-1998; 98US-0081262.
PR 30-APR-1998; 98US-0083670.
PR 19-JUN-1998; 98US-0090096.
PR 22-JUN-1998; 98US-0090216.
PR 11-SEP-1998; 98US-0099957.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA (RODG/) RODGERS K E.
PA (DIZE/) DIZEREGA G.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551209/46.
XX
PT Use of angiotensin and angiotensin type peptides, for mitigating
PT radiation induced tissue damage, improving bone marrow transplantation
PT and promoting megakaryocyte and platelet production -
XX
PS Claim 2; Page 88; 116pp; English.
XX
CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes a method for mitigating
CC radiation induced tissue damage, improving the effectiveness of
CC radiation therapy, to support bone marrow transplantation, and
CC promoting megakaryocyte production and mobilization and platelet
CC production. The method comprises administration of the present peptides.
CC The methods can be used to mitigate radiation induced tissue damage, to
CC improve the effectiveness of radiation therapy, to support bone marrow
CC transplantation, and to promote megakaryocyte production and
CC mobilization and platelet production. They are used particularly in
CC cancer therapy. They can also be used to provide megakaryocytes as
CC vehicles for gene therapy in hematopoietic disorders, by providing a
CC more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
|||||| 
Db 1 drvyih 6

RESULT 9
AAY32721
ID AAY32721 standard; peptide; 6 AA.
XX
AC AAY32721;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-6).
XX
KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
|||||| 
Db 1 drvyih 6

RESULT 10
AAY33775
ID AAY33775 standard; peptide; 6 AA.
XX
AC AAY33775;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(1-6).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US03772.

XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 drvyih 6

RESULT 11
AAY15352
ID AAY15352 standard; peptide; 6 AA.
XX
AC AAY15352;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-6).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX

PS Claim 2; Page 10; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
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Db 1 drvyih 6

RESULT 12
AAY15312
ID AAY15312 standard; peptide; 6 AA.
XX
AC AAY15312;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-6).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a
CC decapeptide called angiotensin I (AI) which is converted to AII by the

```
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY15339).
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 34;  DB 20;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
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Db      1 drvyih 6


RESULT  13
AAB27408
ID   AAB27408 standard; Peptide; 6 AA.
XX
AC   AAB27408;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Angiotensin II analog AII(1-6).
XX
KW   Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW   cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW   heart valve disease; myocarditis; angiotensin.
XX
OS   Synthetic.
XX
PN   WO200053211-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06198.
XX
PR   09-MAR-1999;   99US-0123678.
PR   31-AUG-1999;   99US-0151874.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-611400/58.
XX
PT   Promoting myocyte proliferation and myocardial tissue repair by
PT   contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT   for treating heart attacks, cardiomyopathies, inflammation and
PT   infection -
XX
PS   Claim 2; Page 10; 55pp; English.
XX
CC   The present invention relates to a method of promoting myocyte
CC   proliferation or differentiation by contacting myocytes with an active
CC   agent containing angiotensinogen, angiotensin I and II  (AI, AII), and
CC   angiotensin analogs. The present sequence is an angiotensin II analog
CC   of the invention. The active agents of the invention may be useful for
CC   promoting myocardial tissue repair following myocardial injury and for
CC   treating heart failure in a mammal. Administration to accelerate in
CC   vivo myocyte proliferation and/or to treat myocardial injuries can be
CC   used to treat cardiomyopathies, inflammation, infection, sepsis,
CC   ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC   ischemia and infarction and for improving cardiac output by increasing
CC   stroke volume.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 34;  DB 21;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||
Db      1 drvyih 6


RESULT  14
AAB28106
ID   AAB28106 standard; Peptide; 6 AA.
XX
AC   AAB28106;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Angiotensin II analogue SEQ ID NO: 8.
XX
KW   Wound; scar formation; healing; adhesion formation; AII;
KW   angiotensin II analogue; scar treatment.
XX
OS   Synthetic.
XX
PN   WO200056345-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07669.
XX
PR   23-MAR-1999;   99US-0125707.
PR   16-JUN-1999;   99US-0139541.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-587607/55.
XX
PT   Limiting scar or adhesion formation comprises administering at least
PT   one active agent comprising a peptide -
XX
PS   Claim 2; Page 10; 54pp; English.
XX
CC   The present invention is concerned with peptide analogues of angiotensin
CC   II (AII) which can be used to limit scar and adhesion formation. The
CC   application of AII to wound tissue results in a rapid increase in the
CC   rate of wound healing and causes the proliferation of certain cells, such
CC   as epithelial cells and keratinocytes. Analogues of the protein have been
CC   shown to reduce scar formation, and can be used not only to limit new
CC   scar formation but also to therapeutically treat existing scars. The
CC   wound types include lacerations, burns, punctures, trauma, ulcers,
CC   periodontal conditions, laparotomy and incisional wounds, revision of
CC   hypertrophic scars, genetic hypertrophic scars, keloid scars,
CC   contractures after burns and cosmetic surgical procedures.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 34;  DB 21;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 drvyih 6


RESULT  15
AAY84131
ID   AAY84131 standard; peptide; 6 AA.
XX
AC   AAY84131;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Peptide comprising amino acids 1-6 of angiotensin II.
```

XX
KW Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;
KW analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;
KW congestive heart disease; ischemic myocardial infarction;
KW embryonic development; wound healing; chronic inflammatory disease.
XX
OS Synthetic.
XX
PN WO200009144-A1.
XX
PD 24-FEB-2000.
XX
PF 12-AUG-1999; 99WO-US18374.
XX
PR 13-AUG-1998; 98US-0096414.
PR 18-SEP-1998; 98US-0101024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers K, Dizerega G;
XX
DR WPI; 2000-237409/20.
XX
PT Increasing blood flow to ischemic tissue for minimizing cardiac
PT remodelling and development of congestive heart failure involves
PT administration of an active agent -
XX
PS Claim 2; Page 42; 56pp; English.
XX
CC The present sequence represents an angiotensin II fragment. The
CC specification also describes peptides derived from angiotensinogen,
CC angiotensin I, angiotensin II, angiotensin III, and their analogues.
CC The peptides are used for increasing blood flow to ischemic tissue.
CC The peptides are angiogenesis stimulators. The peptides are useful for
CC increasing blood flow to ischemic tissue by stimulating angiogenesis,
CC and minimizing cardiac remodelling and development of congestive heart
CC disease following a ischemic myocardial infarction. The stimulation of
CC angiogenesis is also useful for embryonic development, wound healing
CC and treating chronic inflammatory disease.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
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Db 1 drvyih 6

Search completed: July 1, 2002, 07:41:55
Job time: 347 sec

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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:00 ; Search time 59.1 Seconds
(without alignments)
2.480 Million cell updates/sec

Title: US-09-723-197-8
Perfect score: 34
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 34 | 100.0 | 6 | 2 | US-08-465-775-8 | Sequence 8, Appli |
| 2 | 34 | 100.0 | 6 | 3 | US-09-208-337-8 | Sequence 8, Appli |
| 3 | 34 | 100.0 | 6 | 3 | US-08-990-664-9 | Sequence 9, Appli |
| 4 | 34 | 100.0 | 6 | 4 | US-09-373-962-8 | Sequence 8, Appli |
| 5 | 34 | 100.0 | 6 | 4 | US-09-245-680-8 | Sequence 8, Appli |
| 6 | 34 | 100.0 | 6 | 4 | US-09-198-806C-8 | Sequence 8, Appli |
| 7 | 34 | 100.0 | 6 | 4 | US-09-352-191-8 | Sequence 8, Appli |
| 8 | 34 | 100.0 | 6 | 4 | US-09-012-400-8 | Sequence 8, Appli |
| 9 | 34 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 10 | 34 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 11 | 34 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
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| 16 | 34 | 100.0 | 7 | 4 | US-09-012-400-4 | Sequence 4, Appli |
| 17 | 34 | 100.0 | 7 | 6 | 5451571-4 | Patent No. 5451571 |
| 18 | 34 | 100.0 | 8 | 1 | US-07-858-842-2 | Sequence 2, Appli |
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| 20 | 34 | 100.0 | 8 | 1 | US-08-184-935-2 | Sequence 2, Appli |
| 21 | 34 | 100.0 | 8 | 1 | US-08-212-433A-29 | Sequence 29, Appl |
| 22 | 34 | 100.0 | 8 | 1 | US-08-185-448-8 | Sequence 8, Appli |
| 23 | 34 | 100.0 | 8 | 1 | US-07-776-272-1 | Sequence 1, Appli |
| 24 | 34 | 100.0 | 8 | 1 | US-08-428-488-21 | Sequence 21, Appl |
| 25 | 34 | 100.0 | 8 | 1 | US-08-337-781-1 | Sequence 1, Appli |
| 26 | 34 | 100.0 | 8 | 1 | US-08-240-711-20 | Sequence 20, Appl |
| 27 | 34 | 100.0 | 8 | 1 | US-08-594-117-1 | Sequence 1, Appli |
| 28 | 34 | 100.0 | 8 | 1 | US-08-520-770-2 | Sequence 2, Appli |
| 29 | 34 | 100.0 | 8 | 1 | US-08-457-753-20 | Sequence 20, Appl |
| 30 | 34 | 100.0 | 8 | 2 | US-08-115-968-1 | Sequence 1, Appli |
| 31 | 34 | 100.0 | 8 | 2 | US-08-115-968-3 | Sequence 3, Appli |
| 32 | 34 | 100.0 | 8 | 2 | US-08-115-968-4 | Sequence 4, Appli |
| 33 | 34 | 100.0 | 8 | 2 | US-08-465-774-1 | Sequence 1, Appli |
| 34 | 34 | 100.0 | 8 | 2 | US-08-360-784B-2 | Sequence 2, Appli |
| 35 | 34 | 100.0 | 8 | 2 | US-08-623-833B-4 | Sequence 4, Appli |
| 36 | 34 | 100.0 | 8 | 2 | US-08-465-775-1 | Sequence 1, Appli |
| 37 | 34 | 100.0 | 8 | 2 | US-08-542-927-3 | Sequence 3, Appli |
| 38 | 34 | 100.0 | 8 | 3 | US-08-716-256-29 | Sequence 29, Appl |
| 39 | 34 | 100.0 | 8 | 3 | US-09-054-308A-2 | Sequence 2, Appli |
| 40 | 34 | 100.0 | 8 | 3 | US-09-280-047-7 | Sequence 7, Appli |
| 41 | 34 | 100.0 | 8 | 3 | US-09-208-337-1 | Sequence 1, Appli |
| 42 | 34 | 100.0 | 8 | 3 | US-08-990-664-1 | Sequence 1, Appli |
| 43 | 34 | 100.0 | 8 | 3 | US-08-990-664-29 | Sequence 29, Appl |
| 44 | 34 | 100.0 | 8 | 3 | US-08-990-664-30 | Sequence 30, Appl |
| 45 | 34 | 100.0 | 8 | 3 | US-08-927-128-16 | Sequence 16, Appl |

ALIGNMENTS

```
RESULT   1
US-08-465-775-8
; Sequence 8, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-8


  Query Match             100.0%;  Score 34;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db       1 DRVYIH 6
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RESULT   2
US-09-208-337-8
; Sequence 8, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-8


  Query Match             100.0%;  Score 34;  DB 3;  Length 6;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 DRVYIH 6


RESULT   3
US-08-990-664-9
; Sequence 9, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-9


  Query Match             100.0%;  Score 34;  DB 3;  Length 6;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   4
US-09-373-962-8
; Sequence 8, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-373-962-8


  Query Match             100.0%;  Score 34;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6
```

```
RESULT   5
US-09-245-680-8
; Sequence 8, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-245-680-8


  Query Match             100.0%;  Score 34;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   6
US-09-198-806C-8
; Sequence 8, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-198-806C-8


  Query Match             100.0%;  Score 34;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   7
US-09-352-191-8
; Sequence 8, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-352-191-8


  Query Match             100.0%;  Score 34;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   8
US-09-012-400-8
; Sequence 8, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-012-400-8


  Query Match             100.0%;  Score 34;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   9
US-08-465-775-4
; Sequence 4, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-4


  Query Match             100.0%;  Score 34;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT  10
US-09-208-337-4
; Sequence 4, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-4


  Query Match             100.0%;  Score 34;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT  11
US-08-990-664-5
; Sequence 5, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-5


  Query Match             100.0%;  Score 34;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
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          ||||||
Db      1 DRVYIH 6


RESULT 12
US-09-373-962-4
; Sequence 4, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-373-962-4


  Query Match             100.0%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT 13
US-09-245-680-4
; Sequence 4, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-245-680-4


  Query Match             100.0%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT 14
US-09-198-806C-4
; Sequence 4, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-198-806C-4


  Query Match             100.0%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT 15
US-09-352-191-4
; Sequence 4, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-352-191-4


  Query Match             100.0%;  Score 34;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:29 ; Search time 69.93 Seconds
(without alignments)
8.244 Million cell updates/sec

Title: US-09-723-197-8
Perfect score: 34
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 2 | 34 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 3 | 34 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 4 | 34 | 100.0 | 476 | 1 | JC2318 | angiotensin precur |
| 5 | 34 | 100.0 | 477 | 1 | ANRT | angiotensin precur |
| 6 | 34 | 100.0 | 477 | 1 | A29978 | angiotensin precur |
| 7 | 34 | 100.0 | 485 | 1 | ANHU | angiotensin precur |
| 8 | 34 | 100.0 | 540 | 2 | S72233 | transcription fact |
| 9 | 33 | 97.1 | 10 | 2 | A60624 | angiotensin I - Ja |
| 10 | 33 | 97.1 | 10 | 2 | A90917 | angiotensin precur |
| 11 | 33 | 97.1 | 10 | 2 | A90345 | angiotensin precur |
| 12 | 33 | 97.1 | 178 | 2 | B42845 | 3-hydroxybutyrate |
| 13 | 32 | 94.1 | 11 | 2 | S07207 | Crinia-angiotensin |
| 14 | 32 | 94.1 | 263 | 2 | F84339 | hypothetical prote |
| 15 | 32 | 94.1 | 460 | 2 | H69095 | carbon monoxide de |
| 16 | 31 | 91.2 | 363 | 2 | A81016 | transcription regu |
| 17 | 30 | 88.2 | 116 | 2 | T03472 | conserved hypothet |
| 18 | 30 | 88.2 | 344 | 2 | A42345 | 3-hydroxybutyrate |
| 19 | 30 | 88.2 | 457 | 2 | JC5422 | FK506-binding prot |
| 20 | 30 | 88.2 | 471 | 2 | B64099 | undecaprenyl-phosp |
| 21 | 30 | 88.2 | 500 | 2 | T19743 | hypothetical prote |
| 22 | 30 | 88.2 | 510 | 2 | E84094 | 2,3-bisphosphoglyc |
| 23 | 30 | 88.2 | 625 | 1 | TBBO | thrombin (EC 3.4.2 |
| 24 | 30 | 88.2 | 970 | 2 | S01352 | type III site-spec |
| 25 | 30 | 88.2 | 1014 | 2 | T18759 | hypothetical prote |
| 26 | 30 | 88.2 | 1069 | 1 | KUHU | ferroxidase (EC 1. |
| 27 | 29 | 85.3 | 111 | 2 | E83566 | hypothetical prote |
| 28 | 29 | 85.3 | 157 | 2 | G00016 | FGF-receptor - com |
| 29 | 29 | 85.3 | 211 | 2 | T42603 | gene 60 protein - |
| 30 | 29 | 85.3 | 212 | 1 | WZBEF2 | gene 60 protein - |
| 31 | 29 | 85.3 | 216 | 2 | T36491 | probable gntR-fami |
| 32 | 29 | 85.3 | 250 | 2 | G81341 | pseudouridylate sy |
| 33 | 29 | 85.3 | 274 | 2 | F81350 | formyltetrahydrofo |
| 34 | 29 | 85.3 | 277 | 2 | E86229 | hypothetical prote |
| 35 | 29 | 85.3 | 281 | 2 | H81315 | probable ribosomal |
| 36 | 29 | 85.3 | 289 | 2 | C96610 | hypothetical prote |
| 37 | 29 | 85.3 | 293 | 2 | E71819 | formyltetrahydrofo |
| 38 | 29 | 85.3 | 293 | 2 | B64699 | formyltetrahydrofo |
| 39 | 29 | 85.3 | 312 | 2 | C82208 | siroheme synthase |
| 40 | 29 | 85.3 | 337 | 2 | T49431 | endozepine related |
| 41 | 29 | 85.3 | 411 | 2 | S14538 | transition protein |
| 42 | 29 | 85.3 | 415 | 2 | I65223 | heparin-binding fi |
| 43 | 29 | 85.3 | 435 | 2 | D71857 | hypothetical prote |
| 44 | 29 | 85.3 | 435 | 2 | B64658 | hypothetical prote |
| 45 | 29 | 85.3 | 444 | 2 | C89768 | conserved hypothet |

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 34; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6
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RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 34; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6
```

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RESULT   3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>


  Query Match            100.0%;  Score 34;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   4
JC2318
angiotensin precursor - sheep
N;Alternate names: angiotensinogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC2318; A25406
R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
A;Reference number: JC2318; MUID:95072318
A;Accession: JC2318
A;Molecule type: mRNA
A;Residues: 1-476 <NAG>
A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 465 as Leu
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A;Title: Purification and characterization of ovine angiotensinogen.
A;Reference number: A25406; MUID:86136099
A;Accession: A25406
A;Molecule type: protein
A;Residues: 25-37,'X',39 <FER>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-476/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin #status predicted <MAT>
F;295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match            100.0%;  Score 34;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     25 DRVYIH 30


RESULT   5
ANRT
```

```
angiotensin precursor - rat
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849
A;Accession: A93945
A;Molecule type: mRNA
A;Residues: 1-477 <OHK>
A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, char
A;Reference number: A90456; MUID:82091819
A;Accession: A90456
A;Molecule type: protein
A;Residues: 25-41 <BOU>
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin I #status experimental <PP1>
F;25-32/Product: angiotensin II #status experimental <PP2>
F;26-32/Product: angiotensin III #status experimental <PP3>
F;295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match            100.0%;  Score 34;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     25 DRVYIH 30


RESULT   6
A29978
angiotensin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29978
R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A;Title: Molecular cloning of the mouse angiotensinogen gene.
A;Reference number: A29978; MUID:88284703
A;Accession: A29978
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-477 <CLO>
A;Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427
C;Genetics:
A;Introns: 277/1; 366/2; 414/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MAT>


  Query Match            100.0%;  Score 34;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
```

```
          ||||||
Db      25 DRVYIH 30


RESULT   7
ANHU
angiotensin precursor [validated] - human
N;Alternate names: angiotensinogen
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1982 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: A35203; A31362; I37168; I37169; A60825; I39462; A90487; A90226; I54281; A01
R;Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,
J. Biol. Chem. 265, 7576-7582, 1990
A;Title: Structure and expression of the human angiotensinogen gene. Identification of a
A;Reference number: A35203; MUID:90237063
A;Accession: A35203
A;Molecule type: DNA
A;Residues: 1-485 <FUK>
A;Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
R;Gaillard, I.; Clauser, E.; Corvol, P.
DNA 8, 87-99, 1989
A;Title: Structure of human angiotensinogen gene.
A;Reference number: A31362; MUID:89170129
A;Accession: A31362
A;Molecule type: DNA
A;Residues: 1-267,'M',269-332,'E',334-485 <GAI>
A;Cross-references: GB:M24686; GB:M24687; GB:M24688
A;Note: the authors translated the codon GAA for residue 333 as Gln
R;Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.
J. Biol. Chem. 269, 28598-28605, 1994
A;Title: Identification of cell type-dependent enhancer core element located in the 3'-d
A;Reference number: I37168; MUID:95050659
A;Accession: I37168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <NIB1>
A;Cross-references: EMBL:X15324; NID:g1197496; PIDN:CAA33385.1; PID:g1197497
A;Accession: I37169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 287-375 <NIB2>
A;Cross-references: EMBL:X15325; NID:g28695
R;Kunapuli, S.P.; Benedict, C.R.; Kumar, A.
Arch. Biochem. Biophys. 254, 642-646, 1987
A;Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.
A;Reference number: A60825; MUID:87212053
A;Accession: A60825
A;Molecule type: mRNA
A;Residues: 32-184 <KUN1>
R;Kunapuli, S.P.; Kumar, A.
Circ. Res. 60, 786-790, 1987
A;Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence o
A;Reference number: I39462; MUID:87244745
A;Accession: I39462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-338 <KUN2>
A;Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181
R;Kageyama, R.; Ohkubo, H.; Nakanishi, S.
Biochemistry 23, 3603-3609, 1984
A;Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ
A;Reference number: A90487; MUID:85000455
A;Accession: A90487
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-485 <KAG>
A;Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640
A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
R;Tewksbury, D.A.; Dart, R.A.; Travis, J.
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
A;Title: The amino terminal amino acid sequence of human angiotensinogen.
A;Reference number: A90226; MUID:81255848
A;Accession: A90226
A;Molecule type: protein
A;Residues: 34-46,'X',48-50,'S',52-57,'D' <TEW>
R;Hixson, J.E.; Powers, P.K.
Hum. Genet. 96, 110-112, 1995
A;Title: Detection and characterization of new mutations in the human angiotensinogen
A;Reference number: I54281; MUID:95331754
A;Accession: I54281
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 176-241,'I',243-267,'M',269-287,'ANLSAG' <HIX>
A;Cross-references: GB:S78529; NID:g999316; PIDN:AAD14287.1; PID:g4261987
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,
o induces thirst.
C;Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
C;Genetics:
A;Gene: GDB:AGT
A;Cross-references: GDB:118750; OMIM:106150
A;Map position: 1q42-1q43
A;Introns: 286/1; 375/2; 423/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>
F;34-485/Product: angiotensinogen #status predicted <MPT>
F;34-43/Product: angiotensin I #status experimental <PP1>
F;34-41/Product: angiotensin II #status experimental <PP2>
F;35-41/Product: angiotensin III #status experimental <PP3>
F;47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 34;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      34 DRVYIH 39


RESULT   8
S72233
transcription factor tbx6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S72233; S72232
R;Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.
submitted to the EMBL Data Library, May 1996
A;Reference number: S72233
A;Accession: S72233
A;Molecule type: mRNA
A;Residues: 1-540 <AGU>
A;Cross-references: EMBL:U57331; NID:g1620601; PIDN:AAC53110.1; PID:g1620602
R;Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B
Genetics 144, 249-254, 1996
A;Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.
A;Reference number: S72230; MUID:97032942
A;Accession: S72232
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 100-280 <AGW>
A;Cross-references: EMBL:U57331
C;Genetics:
A;Gene: tbx6
C;Superfamily: T-box homology
C;Keywords: DNA binding
F;100-282/Domain: T-box homology <TBX>


  Query Match             100.0%;  Score 34;  DB 2;  Length 540;
```

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||||
Db    170 DRVYIH 175
```

RESULT 9
A60624
angiotensin I - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of thes
A;Reference number: A60624; MUID:90284684
A;Accession: A60624
A;Molecule type: protein
A;Residues: 1-10 <TAK>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.1%; Score 33; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

RESULT 10
A90917
angiotensin precursor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90917; A01250
R;Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A;Reference number: A90917; MUID:74127845
A;Accession: A90917
A;Molecule type: protein
A;Residues: 1-10 <NAK>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 33; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

RESULT 11
A90345
angiotensin precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90345; A01250
R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.1%; Score 33; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

RESULT 12
B42845
3-hydroxybutyrate dehydrogenase (EC 1.1.1.30) - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Sep-1998
C;Accession: B42845
R;Marks, A.R.; McIntyre, J.O.; Duncan, T.M.; Erdjument-Bromage, H.; Tempst, P.; Fleis
J. Biol. Chem. 267, 15459-15463, 1992
A;Title: Molecular cloning and characterization of (R)-3-hydroxybutyrate dehydrogenas
A;Reference number: A42845; MUID:92348395
A;Accession: B42845
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-178 <MAR>
A;Experimental source: heart
A;Note: sequence extracted from NCBI backbone (NCBIP:109586, NCBIP:109588, NCBIP:1095
C;Superfamily: retinol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: mitochondrion; oxidoreductase
F;10-108/Domain: short-chain alcohol dehydrogenase homology (fragments) <SADH>

Query Match 97.1%; Score 33; DB 2; Length 178;
Best Local Similarity 83.3%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||:|||
Db    173 DRIYIH 178
```

RESULT 13
S07207
Crinia-angiotensin, skin - frog (Crinia georgiana)
C;Species: Crinia georgiana
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C;Accession: S07207
R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A;Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II
A;Reference number: S07207; MUID:80024575
A;Accession: S07207
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides

Query Match 94.1%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 0.57;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIH 6
          ||:|:|
Db      4 DRIYVH 9
```

RESULT 14
F84339
hypothetical protein Vng1886c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84339
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: F84339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <STO>
A;Cross-references: GB:AE004437; NID:g10581327; PIDN:AAG20082.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1886C

Query Match 94.1%; Score 32; DB 2; Length 263;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 DRVYIH 6
             ||||:|
Db     215 DRVYLH 220
```

RESULT 15
H69095
carbon monoxide dehydrogenase, alpha subunit - Methanobacterium thermoautotrophicum (str
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69095
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514
A;Accession: H69095
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-460 <MTH>
A;Cross-references: GB:AE000928; GB:AE000666; NID:g2622835; PIDN:AAB86182.1; PID:g262284
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1710

Query Match 94.1%; Score 32; DB 2; Length 460;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 DRVYIH 6
             ||||:|
Db     262 DRVYLH 267
```

Search completed: July 1, 2002, 07:46:29
Job time: 450 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:08 ; Search time 34.05 Seconds
(without alignments)
6.823 Million cell updates/sec

Title: US-09-723-197-8
Perfect score: 34
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 34 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 3 | 34 | 100.0 | 436 | 1 | TBX6_HUMAN | O95947 homo sapien |
| 4 | 34 | 100.0 | 476 | 1 | ANGT_SHEEP | P20757 ovis aries |
| 5 | 34 | 100.0 | 477 | 1 | ANGT_MOUSE | P11859 mus musculu |
| 6 | 34 | 100.0 | 477 | 1 | ANGT_RAT | P01015 rattus norv |
| 7 | 34 | 100.0 | 485 | 1 | ANGT_HUMAN | P01019 homo sapien |
| 8 | 34 | 100.0 | 540 | 1 | TBX6_MOUSE | P70327 mus musculu |
| 9 | 33 | 97.1 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 10 | 33 | 97.1 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 11 | 33 | 97.1 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 12 | 33 | 97.1 | 178 | 1 | BDH_BOVIN | Q02337 bos taurus |
| 13 | 32 | 94.1 | 11 | 1 | ANGT_CRIGE | P09037 crinia geor |
| 14 | 30 | 88.2 | 344 | 1 | BDH_RAT | P29147 rattus norv |
| 15 | 30 | 88.2 | 456 | 1 | FKB5_MOUSE | Q64378 mus musculu |
| 16 | 30 | 88.2 | 457 | 1 | FKB5_HUMAN | Q13451 homo sapien |
| 17 | 30 | 88.2 | 471 | 1 | Y872_HAEIN | Q57491 haemophilus |
| 18 | 30 | 88.2 | 625 | 1 | THRB_BOVIN | P00735 bos taurus |
| 19 | 30 | 88.2 | 970 | 1 | T3RE_BPP1 | P08764 bacteriopha |
| 20 | 30 | 88.2 | 1062 | 1 | CERU_MOUSE | Q61147 mus musculu |
| 21 | 30 | 88.2 | 1065 | 1 | CERU_HUMAN | P00450 homo sapien |
| 22 | 29 | 85.3 | 212 | 1 | UL03_HSVEB | P28942 equine herp |
| 23 | 29 | 85.3 | 376 | 1 | FA10_TROCA | P81428 tropidechis |
| 24 | 29 | 85.3 | 457 | 1 | FKB4_MOUSE | P30416 mus musculu |
| 25 | 29 | 85.3 | 457 | 1 | FKB4_RABIT | P27124 oryctolagus |
| 26 | 29 | 85.3 | 458 | 1 | FKB4_HUMAN | Q02790 homo sapien |
| 27 | 29 | 85.3 | 654 | 1 | BFR2_HUMAN | Q01742 homo sapien |
| 28 | 29 | 85.3 | 659 | 1 | POL_CERV | P05400 carnation e |
| 29 | 29 | 85.3 | 801 | 1 | FGR3_MOUSE | Q61851 mus musculu |
| 30 | 29 | 85.3 | 802 | 1 | FGR4_HUMAN | P22455 homo sapien |
| 31 | 29 | 85.3 | 806 | 1 | CEK2_CHICK | P18460 gallus gall |
| 32 | 29 | 85.3 | 806 | 1 | FGR3_HUMAN | P22607 homo sapien |
| 33 | 29 | 85.3 | 808 | 1 | FGR4_MOUSE | Q03142 mus musculu |
| 34 | 29 | 85.3 | 813 | 1 | FGR2_XENLA | Q03364 xenopus lae |
| 35 | 29 | 85.3 | 821 | 1 | FGR2_HUMAN | P21802 homo sapien |
| 36 | 29 | 85.3 | 821 | 1 | FGR2_MOUSE | P21803 mus musculu |
| 37 | 29 | 85.3 | 823 | 1 | CEK3_CHICK | P18461 gallus gall |
| 38 | 29 | 85.3 | 1036 | 1 | YQB6_CAEEL | Q09259 caenorhabdi |
| 39 | 29 | 85.3 | 2344 | 1 | POLN_RHDV | P27410 rabbit hemo |
| 40 | 28 | 82.4 | 144 | 1 | UP03_ECOLI | P37903 escherichia |
| 41 | 28 | 82.4 | 161 | 1 | YG22_HAEIN | P44275 haemophilus |
| 42 | 28 | 82.4 | 224 | 1 | Y042_HAEIN | P43930 haemophilus |
| 43 | 28 | 82.4 | 305 | 1 | ENDA_ARCFU | O29362 archaeoglob |
| 44 | 28 | 82.4 | 375 | 1 | NUEM_NEUCR | P25284 neurospora |
| 45 | 28 | 82.4 | 501 | 1 | TX18_HUMAN | O95935 homo sapien |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 34; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6
||||||
Db 1 DRVYIH 6

RESULT 2
ANGT_HORSE
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";

```
RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db      1 DRVYIH 6


RESULT   3
TBX6_HUMAN
ID   TBX6_HUMAN     STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
RN   [2]
RP   SEQUENCE OF 135-272 FROM N.A.
RC   TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db    170 DRVYIH 175


RESULT   4
ANGT_SHEEP
ID   ANGT_SHEEP     STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    476       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      25 DRVYIH 30


RESULT   5
ANGT_MOUSE
ID   ANGT_MOUSE     STANDARD;      PRT;   477 AA.
AC   P11859;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88284703; PubMed=3397061;
RA   Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT   "Molecular cloning of the mouse angiotensinogen gene.";
RL   Genomics 2:240-248(1988).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF045887; AAC01765.1; -.
DR   EMBL; AF045886; AAC01765.1; JOINED.
DR   EMBL; AF045885; AAC01765.1; JOINED.
DR   EMBL; AF045884; AAC01765.1; JOINED.
DR   PIR; A29978; A29978.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51990 MW;  A877F4029F338607 CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      25 DRVYIH 30


RESULT   6
ANGT_RAT
ID   ANGT_RAT       STANDARD;      PRT;   477 AA.
AC   P01015;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR;
RX   MEDLINE=83169849; PubMed=6572971;
RA   Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA   Nakanishi S.;
RT   "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN   [2]
RP   SEQUENCE OF 25-34.
RX   MEDLINE=73060322; PubMed=4344907;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. II. Structure of rat
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 20:1579-1581(1972).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L00094; AAA98779.1; -.
DR   EMBL; L00091; AAA98779.1; JOINED.
DR   EMBL; L00092; AAA98779.1; JOINED.
DR   EMBL; L00093; AAA98779.1; JOINED.
DR   PIR; A01251; ANRT.
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DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51981 MW;  689051A5788D693D CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     25 DRVYIH 30


RESULT   7
ANGT_HUMAN
ID   ANGT_HUMAN     STANDARD;      PRT;   485 AA.
AC   P01019; Q16358; Q16359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89170129; PubMed=2924688;
RA   Gaillard I., Clauser E., Corvol P.;
RT   "Structure of human angiotensinogen gene.";
RL   DNA 8:87-99(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85000455; PubMed=6089875;
RA   Kageyama R., Ohkubo H., Nakanishi S.;
RT   "Primary structure of human preangiotensinogen deduced from the
RT   cloned cDNA sequence.";
RL   Biochemistry 23:3603-3609(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90237063; PubMed=1692023;
RA   Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA   Murakami K.;
RT   "Structure and expression of the human angiotensinogen gene.
RT   Identification of a unique and highly active promoter.";
RL   J. Biol. Chem. 265:7576-7582(1990).
RN   [4]
RP   SEQUENCE OF 1-338 FROM N.A.
RX   MEDLINE=87244745; PubMed=2885106;
RA   Kunapuli S.P., Kumar A.;
RT   "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT   presence of its mRNA in rat heart.";
RL   Circ. Res. 60:786-790(1987).
RN   [5]
RP   SEQUENCE OF 34-45, AND SUBUNITS.
RC   TISSUE=Serum;
RX   MEDLINE=95293954; PubMed=7539791;
RA   Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA   Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT   "Identification of angiotensinogen and complement C3dg as novel
RT   proteins binding the proform of eosinophil major basic protein in
RT   human pregnancy serum and plasma.";
RL   J. Biol. Chem. 270:13645-13651(1995).
RN   [6]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=69014170; PubMed=4300938;
RA   Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT   "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL   Biochim. Biophys. Acta 168:106-112(1968).
RN   [7]
RP   STRUCTURE BY NMR OF ANGIOTENSIN II.
RX   MEDLINE=98151281; PubMed=9492317;
RA   Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT   "The octapeptide angiotensin II adopts a well-defined structure in a
RT   phospholipid environment.";
RL   Eur. J. Biochem. 251:448-453(1998).
RN   [8]
RP   VARIANTS MET-207; THR-268 AND CYS-281.
RX   MEDLINE=93008239; PubMed=1394429;
RA   Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA   Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA   Lalouel J.-M., Corvol P.;
RT   "Molecular basis of human hypertension: role of angiotensinogen.";
RL   Cell 71:169-180(1992).
RN   [9]
RP   VARIANT THR-268.
RX   MEDLINE=93291876; PubMed=8513325;
RA   Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA   Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
RA   Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT   "A molecular variant of angiotensinogen associated with
RT   preeclampsia.";
RL   Nat. Genet. 4:59-61(1993).
RN   [10]
RP   VARIANTS ILE-242; ARG-244 AND CYS-281.
RX   MEDLINE=95331754; PubMed=7607642;
RA   Hixson J.E., Powers P.K.;
RT   "Detection and characterization of new mutations in the human
RT   angiotensinogen gene (AGT).";
RL   Hum. Genet. 96:110-112(1995).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
CC       heterotetramer with the proform of PRG2 and as a complex (probably
CC       a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
CC       ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
CC       (PIH) (PREECLAMPSIA).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02215; AAA51731.1; -.
DR   EMBL; M24689; AAA51679.1; -.
DR   EMBL; M24686; AAA51679.1; JOINED.
DR   EMBL; M24687; AAA51679.1; JOINED.
DR   EMBL; M24688; AAA51679.1; JOINED.
DR   EMBL; X15324; CAA33385.1; -.
DR   EMBL; X15325; CAA33385.1; JOINED.
DR   EMBL; X15326; CAA33385.1; JOINED.
DR   EMBL; X15327; CAA33385.1; JOINED.
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DR   EMBL; M69110; AAA52282.1; -.
DR   EMBL; S78529; AAD14287.1; -.
DR   EMBL; S78530; AAD14288.1; -.
DR   PIR; A01249; ANHU.
DR   PIR; A31362; A31362.
DR   PIR; A35203; A35203.
DR   SWISS-2DPAGE; P01019; HUMAN.
DR   MIM; 106150; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW   Disease mutation; Polymorphism.
FT   SIGNAL       1     33
FT   CHAIN       34    485       ANGIOTENSINOGEN.
FT   PEPTIDE     34     43       ANGIOTENSIN I.
FT   PEPTIDE     34     41       ANGIOTENSIN II.
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    207    207       T -> M.
FT                               /FTId=VAR_007093.
FT   VARIANT    242    242       T -> I (IN HYPERTENSION).
FT                               /FTId=VAR_007094.
FT   VARIANT    244    244       L -> R (IN HYPERTENSION).
FT                               /FTId=VAR_007095.
FT   VARIANT    268    268       M -> T (IN HYPERTENSION).
FT                               /FTId=VAR_007096.
FT   VARIANT    281    281       Y -> C (IN HYPERTENSION).
FT                               /FTId=VAR_007097.
FT   CONFLICT   333    333       Q -> E (IN REF. 1).
SQ   SEQUENCE   485 AA;  53154 MW;  5026C2DFB2DD236E CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      34 DRVYIH 39


RESULT   8
TBX6_MOUSE
ID   TBX6_MOUSE     STANDARD;      PRT;   540 AA.
AC   P70327;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97032942; PubMed=8878690;
RA   Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA   Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT   "Evolution of mouse T-box genes by tandem duplication and cluster
RT   dispersion.";
RL   Genetics 144:249-254(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastrula;
RX   MEDLINE=97115702; PubMed=8954725;
RA   Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT   "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT   gastrulation.";
RL   Dev. Biol. 180:534-542(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=98140705; PubMed=9490412;
RA   Chapman D.L., Papaioannou V.E.;
RT   "Three neural tubes in mouse embryos with mutations in the T-box gene
RT   Tbx6.";
RL   Nature 391:695-697(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC       MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC       DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC       PATHWAY.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC       STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC       MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC       PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC       AS THE SOURCE OF MESODERM.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57331; AAC53110.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:102539; Tbx6.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       61     64       POLY-ALA.
FT   DOMAIN       79     82       POLY-PRO.
FT   DNA_BIND    100    273       T-BOX.
SQ   SEQUENCE   540 AA;  58628 MW;  BC834CE2745E8E61 CRC64;


  Query Match             100.0%;  Score 34;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db     170 DRVYIH 175


RESULT   9
ANG1_BOTJA
ID   ANG1_BOTJA     STANDARD;      PRT;    10 AA.
AC   Q10581;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Angiotensin-like peptide I (Fragment).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
```

```
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=96208932; PubMed=8829801;
RA   Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1308 MW;  CEF50DD761F2DB42 CRC64;
```

```
  Query Match           97.1%;  Score 33;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 0.19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

```
RESULT  10
ANGT_BOVIN
ID   ANGT_BOVIN     STANDARD;      PRT;    10 AA.
AC   P01017;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RA   Elliott D.F., Peart W.S.;
RT   "The amino acid sequence in a hypertensin.";
RL   Biochem. J. 65:246-254(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90345; A90345.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1282 MW;  CEEFBDD761F2DB42 CRC64;
```

```
  Query Match           97.1%;  Score 33;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 0.19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

```
RESULT  11
ANGT_CHICK
ID   ANGT_CHICK     STANDARD;      PRT;    10 AA.
AC   P01018;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken;
RX   MEDLINE=74127845; PubMed=4361802;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. 3. Structure of fowl
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 21:2085-2087(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=90284684; PubMed=2191893;
RA   Takei Y., Hasegawa Y.;
RT   "Vasopressor and depressor effects of native angiotensins and
RT   inhibition of these effects in the Japanese quail.";
RL   Gen. Comp. Endocrinol. 79:12-22(1990).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90917; A90917.
DR   PIR; A60624; A60624.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1232 MW;  CEFBEDD761F2DB42 CRC64;
```

```
  Query Match           97.1%;  Score 33;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 0.19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6
```

```
RESULT  12
BDH_BOVIN
ID   BDH_BOVIN      STANDARD;      PRT;   178 AA.
AC   Q02337;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)
DE   (3-hydroxybutyrate dehydrogenase) (Fragments).
GN   BDH.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
```

```
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=92348395; PubMed=1639787;
RA   Marks A.R., McIntyre J.O., Duncan T.M., Erdjument-Bromage H.,
RA   Tempst P., Fleischer S.;
RT   "Molecular cloning and characterization of (R)-3-hydroxybutyrate
RT   dehydrogenase from human heart.";
RL   J. Biol. Chem. 267:15459-15463(1992).
RN   [2]
RP   SEQUENCE OF 69-80 AND 127-143.
RC   TISSUE=Heart;
RX   MEDLINE=86295814; PubMed=3527172;
RA   Prasad P.V., Hatefi Y.;
RT   "Amino acid sequences of two tryptic peptides from D(-)-beta-
RT   hydroxybutyrate dehydrogenase radiolabeled at essential carboxyl and
RT   sulfhydryl groups.";
RL   Biochem. Int. 12:941-949(1986).
CC   -!- CATALYTIC ACTIVITY: (R)-3-hydroxybutanoate + NAD(+) = acetoacetate
CC       + NADH.
CC   -!- COFACTOR: REQUIRES PHOSPHATIDYLCHOLINE AS AN ALLOSTERIC ACTIVATOR
CC       FOR ENZYMIC ACTIVITY.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC   -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC       (SDR) FAMILY.
DR   PIR; B42845; B42845.
DR   HSSP; P14061; 1IOL.
DR   InterPro; IPR002198; ADH_short.
DR   PROSITE; PS00061; ADH_SHORT; PARTIAL.
KW   Oxidoreductase; NAD; Mitochondrion; Inner membrane.
FT   NON_CONS      43      44
FT   NON_CONS      80      81
FT   NON_CONS      99     100
FT   NON_CONS     126     127
FT   NON_CONS     164     165
SQ   SEQUENCE   178 AA;  19303 MW;  399BF046FAAD6CD5 CRC64;


  Query Match             97.1%;  Score 33;  DB 1;  Length 178;
  Best Local Similarity   83.3%;  Pred. No. 3.2;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||:|||
Db    173 DRIYIH 178


RESULT  13
ANGT_CRIGE
ID   ANGT_CRIGE     STANDARD;      PRT;    11 AA.
AC   P09037;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Crinia-angiotensin II.
OS   Crinia georgiana (Quacking frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Crinia.
OX   NCBI_TaxID=8374;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE=80024575; PubMed=488254;
RA   Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT   "Amino acid composition and sequence of crinia-angiotensin, an
RT   angiotensin II-like endecapeptide from the skin of the Australian
RT   frog Crinia georgiana.";
RL   Experientia 35:1132-1133(1979).
DR   PIR; S07207; S07207.
KW   Vasoconstrictor.
SQ   SEQUENCE   11 AA;  1271 MW;  8A0921F7DB50440A CRC64;


  Query Match             94.1%;  Score 32;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 0.34;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||:|:|
Db      4 DRIYVH 9


RESULT  14
BDH_RAT
ID   BDH_RAT        STANDARD;      PRT;   344 AA.
AC   P29147;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor
DE   (EC 1.1.1.30) (BDH) (3-hydroxybutyrate dehydrogenase).
GN   BDH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX   MEDLINE=92232670; PubMed=1567834;
RA   Churchill P., Hempel J., Romovacek H., Zhang W.W., Churchill S.,
RA   Brennan M.;
RT   "Primary structure of rat liver D-beta-hydroxybutyrate dehydrogenase
RT   from cDNA and protein analyses: a short-chain alcohol
RT   dehydrogenase.";
RL   Biochemistry 31:3793-3799(1992).
CC   -!- CATALYTIC ACTIVITY: (R)-3-hydroxybutanoate + NAD(+) = acetoacetate
CC       + NADH.
CC   -!- COFACTOR: REQUIRES PHOSPHATIDYLCHOLINE FOR ENZYMATIC ACTIVITY.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC   -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC       (SDR) FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M89902; AAB59684.1; -.
DR   PIR; A42345; A42345.
DR   HSSP; P14061; 1FDS.
DR   InterPro; IPR002198; ADH_short.
DR   Pfam; PF00106; adh_short; 1.
DR   PRINTS; PR00080; SDRFAMILY.
DR   PROSITE; PS00061; ADH_SHORT; 1.
KW   Oxidoreductase; NAD; Mitochondrion; Transit peptide.
FT   TRANSIT       1      47       MITOCHONDRION.
FT   CHAIN        48     344       D-BETA-HYDROXYBUTYRATE DEHYDROGENASE.
FT   NP_BIND      60      84       NAD (BY SIMILARITY).
FT   ACT_SITE    209     209       BY SIMILARITY.
SQ   SEQUENCE   344 AA;  38347 MW;  EBC76565FFD111DF CRC64;


  Query Match             88.2%;  Score 30;  DB 1;  Length 344;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          |::|||
Db    339 DKIYIH 344
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RESULT 15
FKB5_MOUSE
ID   FKB5_MOUSE     STANDARD;      PRT;   456 AA.
AC   Q64378;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans
DE   isomerase) (EC 5.2.1.8) (PPiase) (Rotamase).
GN   FKBP5 OR FKBP51.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96074651; PubMed=7479941;
RA   Yeh W.-C., Li T.-K., Bierer B.E., McKnight S.L.;
RT   "Identification and characterization of an immunophilin expressed
RT   during the clonal expansion phase of adipocyte differentiation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Thymus;
RX   MEDLINE=95349606; PubMed=7542743;
RA   Baughman G., Wiederrecht G.J., Campbell N.F., Martin M.M.,
RA   Bourgeois S.;
RT   "FKBP51, a novel T-cell-specific immunophilin capable of calcineurin
RT   inhibition.";
RL   Mol. Cell. Biol. 15:4395-4402(1995).
CC   -!- FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC       PEPTIDE BONDS IN OLIGOPEPTIDES.
CC   -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE
CC       LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
CC       DURING ADIPOCYTE DIFFERENTIATION.
CC   -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
CC       FKBP-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U36220; AAA89162.1; -.
DR   EMBL; U16959; AAA86983.1; -.
DR   HSSP; P27124; 1ROT.
DR   MGD; MGI:104670; Fkbp5.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 3.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
KW   Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
FT   DOMAIN       50    138       PPIASE, FKBP-TYPE 1.
FT   DOMAIN      165    251       PPIASE, FKBP-TYPE 2.
FT   REPEAT      268    301       TPR 1.
FT   REPEAT      317    350       TPR 2.
FT   REPEAT      352    384       TPR 3.
SQ   SEQUENCE   456 AA;  50966 MW;  8FD0C9B61478EB46 CRC64;
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Query Match 88.2%; Score 30; DB 1; Length 456;

Best Local Similarity 66.7%; Pred. No. 36;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIH 6
           |:||:|
Db      51 DKVYVH 56
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Search completed: July 1, 2002, 07:47:09
Job time: 475 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:12 ; Search time 122.73 Seconds
(without alignments)
8.457 Million cell updates/sec

Title: US-09-723-197-8
Perfect score: 34
Sequence: 1 DRVYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 2 | 34 | 100.0 | 245 | 6 | Q95J13 | Q95j13 pan troglod |
| 3 | 34 | 100.0 | 295 | 4 | Q9HA44 | Q9ha44 homo sapien |
| 4 | 34 | 100.0 | 461 | 11 | Q9D2V0 | Q9d2v0 mus musculu |
| 5 | 34 | 100.0 | 477 | 4 | Q96FD5 | Q96fd5 homo sapien |
| 6 | 34 | 100.0 | 485 | 4 | Q96F91 | Q96f91 homo sapien |
| 7 | 34 | 100.0 | 485 | 6 | Q9GLP7 | Q9glp7 pan troglod |
| 8 | 34 | 100.0 | 485 | 6 | Q9GLP6 | Q9glp6 gorilla gor |
| 9 | 34 | 100.0 | 485 | 6 | Q9GLN8 | Q9gln8 pan troglod |
| 10 | 34 | 100.0 | 486 | 6 | Q9TSZ0 | Q9tsz0 callithrix |
| 11 | 33 | 97.1 | 10 | 13 | Q9PS07 | Q9ps07 alligator m |
| 12 | 33 | 97.1 | 457 | 6 | Q9XSH5 | Q9xsh5 saimiri bol |
| 13 | 32 | 94.1 | 263 | 17 | Q9HNY8 | Q9hny8 halobacteri |
| 14 | 32 | 94.1 | 460 | 17 | O27745 | O27745 methanother |
| 15 | 32 | 94.1 | 546 | 12 | Q91HA5 | Q91ha5 rinderpest |
| 16 | 32 | 94.1 | 808 | 1 | Q52045 | Q52045 halobacteri |
| 17 | 31 | 91.2 | 171 | 17 | Q971G2 | Q971g2 sulfolobus |
| 18 | 31 | 91.2 | 363 | 16 | Q9JXJ6 | Q9jxj6 neisseria m |
| 19 | 30 | 88.2 | 116 | 2 | O68039 | O68039 rhodobacter |
| 20 | 30 | 88.2 | 247 | 16 | Q988V3 | Q988v3 rhizobium l |
| 21 | 30 | 88.2 | 388 | 5 | Q9N508 | Q9n508 caenorhabdi |
| 22 | 30 | 88.2 | 388 | 5 | Q9NAL0 | Q9nal0 caenorhabdi |
| 23 | 30 | 88.2 | 420 | 10 | Q94E08 | Q94e08 oryza sativ |
| 24 | 30 | 88.2 | 457 | 6 | Q9XT11 | Q9xt11 aotus nancy |
| 25 | 30 | 88.2 | 457 | 6 | Q9XSI2 | Q9xsi2 saguinus oe |
| 26 | 30 | 88.2 | 457 | 6 | Q95L05 | Q95l05 cercopithec |
| 27 | 30 | 88.2 | 473 | 2 | Q9AIX7 | Q9aix7 azoarcus ev |
| 28 | 30 | 88.2 | 500 | 5 | Q18475 | Q18475 caenorhabdi |
| 29 | 30 | 88.2 | 510 | 16 | Q9K716 | Q9k716 bacillus ha |
| 30 | 30 | 88.2 | 986 | 5 | Q9N9W3 | Q9n9w3 haemonchus |
| 31 | 30 | 88.2 | 1014 | 5 | Q17505 | Q17505 caenorhabdi |
| 32 | 30 | 88.2 | 1048 | 6 | Q9XT27 | Q9xt27 ovis aries |
| 33 | 30 | 88.2 | 1590 | 5 | Q9V7E3 | Q9v7e3 drosophila |
| 34 | 29 | 85.3 | 56 | 13 | Q91995 | Q91995 xenopus lae |
| 35 | 29 | 85.3 | 57 | 13 | Q08556 | Q08556 phasianidae |
| 36 | 29 | 85.3 | 68 | 13 | Q9YI21 | Q9yi21 gallus gall |
| 37 | 29 | 85.3 | 111 | 16 | Q9I5S2 | Q9i5s2 pseudomonas |
| 38 | 29 | 85.3 | 129 | 11 | Q63000 | Q63000 rattus norv |
| 39 | 29 | 85.3 | 153 | 2 | O86161 | O86161 campylobact |
| 40 | 29 | 85.3 | 157 | 6 | Q28332 | Q28332 callithrix |
| 41 | 29 | 85.3 | 157 | 6 | Q28111 | Q28111 bos taurus |
| 42 | 29 | 85.3 | 164 | 2 | Q9R6J1 | Q9r6j1 agrobacteri |
| 43 | 29 | 85.3 | 209 | 13 | Q9DE16 | Q9de16 brachydanio |
| 44 | 29 | 85.3 | 211 | 12 | O39300 | O39300 equine herp |
| 45 | 29 | 85.3 | 216 | 2 | Q9XA67 | Q9xa67 streptomyce |

ALIGNMENTS

RESULT 1
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIH 6

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          ||||||
Db      1 DRVYIH 6


RESULT   2
Q95J13
ID   Q95J13      PRELIMINARY;      PRT;   245 AA.
AC   Q95J13;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
GN   REN.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=504, AND 505;
RA   Satta Y.;
RT   "Comparison of DNA and protein polymorphims between humans and
RT   chimpanzees.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062027; BAB55856.1; -.
DR   EMBL; AB062028; BAB55857.1; -.
FT   NON_TER     245     245
SQ   SEQUENCE   245 AA;  26317 MW;  E0092390B9803E0B CRC64;


  Query Match             100.0%;  Score 34;  DB 6;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     34 DRVYIH 39


RESULT   3
Q9HA44
ID   Q9HA44      PRELIMINARY;      PRT;   295 AA.
AC   Q9HA44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE   TRANSCRIPTION FACTOR TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022330; BAB14014.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33197 MW;  F2BD3E53E0ED21E0 CRC64;


  Query Match             100.0%;  Score 34;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db    170 DRVYIH 175


RESULT   4
Q9D2V0
ID   Q9D2V0      PRELIMINARY;      PRT;   461 AA.
AC   Q9D2V0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018763; BAB31393.1; -.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
SQ   SEQUENCE   461 AA;  50327 MW;  446EB0881079251F CRC64;


  Query Match             100.0%;  Score 34;  DB 11;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     30 DRVYIH 35


RESULT   5
Q96FD5
ID   Q96FD5      PRELIMINARY;      PRT;   477 AA.
AC   Q96FD5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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DE   SIMILAR TO ANGIOTENSINOGEN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011231; AAH11231.1; -.
SQ   SEQUENCE   477 AA;  51985 MW;  AB79B8B70592FDE2 CRC64;


  Query Match             100.0%;  Score 34;  DB 4;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      25 DRVYIH 30


RESULT   6
Q96F91
ID   Q96F91      PRELIMINARY;      PRT;   485 AA.
AC   Q96F91;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE
DE   A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 8).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011519; AAH11519.1; -.
SQ   SEQUENCE   485 AA;  53114 MW;  50BA5E9DCD4C8E7F CRC64;


  Query Match             100.0%;  Score 34;  DB 4;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      34 DRVYIH 39


RESULT   7
Q9GLP7
ID   Q9GLP7      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188487; AAG29056.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53140 MW;  49EFB54AF31F8ADC CRC64;


  Query Match             100.0%;  Score 34;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      34 DRVYIH 39


RESULT   8
Q9GLP6
ID   Q9GLP6      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188488; AAG29057.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53186 MW;  53BC9235271C8255 CRC64;


  Query Match             100.0%;  Score 34;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIH 6
           ||||||
Db      34 DRVYIH 39


RESULT   9
Q9GLN8
ID   Q9GLN8      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLN8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=20469400; PubMed=11013071;
RA   Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA   Jeunemaitre X.;
RT   "Human-Chimpanzee DNA sequence variation in the four major genes of
RT   the renin angiotensin system.";
RL   Genomics 69:14-26(2000).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF193461; AAG30306.1; -.
DR   EMBL; AF193458; AAG30306.1; JOINED.
DR   EMBL; AF193459; AAG30306.1; JOINED.
DR   EMBL; AF193460; AAG30306.1; JOINED.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53110 MW;  C14C67E49A53F05F CRC64;

  Query Match           100.0%;  Score 34;  DB 6;  Length 485;
  Best Local Similarity  100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     34 DRVYIH 39


RESULT  10
Q9TSZ0
ID   Q9TSZ0      PRELIMINARY;      PRT;   486 AA.
AC   Q9TSZ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR.
GN   ANGT.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065005; PubMed=10598135;
RA   Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;
RT   "Cloning and characterization of marmoset renin: comparison with human
RT   renin.";
RL   J. Cardiovasc. Pharmacol. 34:893-897(1999).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AJ132343; CAB64880.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin; Signal.
FT   SIGNAL       1     33       POTENTIAL.
FT   CHAIN       34    486       ANGIOTENSINOGEN.
SQ   SEQUENCE   486 AA;  53374 MW;  5408129B2F71FB8B CRC64;

  Query Match           100.0%;  Score 34;  DB 6;  Length 486;
  Best Local Similarity  100.0%;  Pred. No. 21;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||||
Db     34 DRVYIH 39
```

```
RESULT  11
Q9PS07
ID   Q9PS07      PRELIMINARY;      PRT;    10 AA.
AC   Q9PS07;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ANGIOTENSIN I, ANG I.
OS   Alligator mississippiensis (American alligator).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX   NCBI_TaxID=8496;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93307610; PubMed=8319878;
RA   Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA   Stephens G.A., Sakakibara S.;
RT   "New angiotensin I isolated from a reptile, Alligator
RT   mississippiensis.";
RL   Gen. Comp. Endocrinol. 90:214-219(1993).
SQ   SEQUENCE   10 AA;  1216 MW;  CEE38DD761F2DB42 CRC64;

  Query Match           97.1%;  Score 33;  DB 13;  Length 10;
  Best Local Similarity  83.3%;  Pred. No. 0.66;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db      1 DRVYVH 6


RESULT  12
Q9XSH5
ID   Q9XSH5      PRELIMINARY;      PRT;   457 AA.
AC   Q9XSH5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FK506-BINDING PROTEIN FKBP51.
OS   Saimiri boliviensis (Bolivian squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=27679;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20539274; PubMed=11089542;
RA   Denny W.B., Valentine D.L., Reynolds P.D., Smith D.F., Scammell J.G.;
RT   "Squirrel Monkey Immunophilin FKBP51 Is a Potent Inhibitor of
RT   Glucocorticoid Receptor Binding.";
RL   Endocrinology 141:4107-4113(2000).
DR   EMBL; AF140759; AAD32678.1; -.
DR   HSSP; P27124; 1ROT.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ   SEQUENCE   457 AA;  51169 MW;  DFF9E1D81F7759A8 CRC64;

  Query Match           97.1%;  Score 33;  DB 6;  Length 457;
  Best Local Similarity  83.3%;  Pred. No. 33;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db     51 DRVYVH 56


RESULT  13
```

```
Q9HNY8
ID   Q9HNY8      PRELIMINARY;      PRT;   263 AA.
AC   Q9HNY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   VNG1886C.
GN   VNG1886C.
OS   Halobacterium sp. (strain NRC-1).
OC   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC   Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR   EMBL; AE005087; AAG20082.1; -.
DR   InterPro; IPR002831; DUF118.
DR   Pfam; PF01978; DUF118; 1.
DR   ProDom; PD006327; DUF118; 1.
KW   Complete proteome.
SQ   SEQUENCE   263 AA;  29005 MW;  22EB839F64CE8542 CRC64;


  Query Match             94.1%;  Score 32;  DB 17;  Length 263;
  Best Local Similarity   83.3%;  Pred. No. 31;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db    215 DRVYLH 220


RESULT  14
O27745
ID   O27745      PRELIMINARY;      PRT;   460 AA.
AC   O27745;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   CARBON MONOXIDE DEHYDROGENASE, ALPHA SUBUNIT.
GN   MTH1710.
OS   Methanothermobacter thermautotrophicus.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
DR   EMBL; AE000928; AAB86182.1; -.
KW   Complete proteome.
SQ   SEQUENCE   460 AA;  51737 MW;  DB4D50693D154BDA CRC64;


  Query Match             94.1%;  Score 32;  DB 17;  Length 460;
  Best Local Similarity   83.3%;  Pred. No. 56;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db    262 DRVYLH 267


RESULT  15
Q91HA5
ID   Q91HA5      PRELIMINARY;      PRT;   546 AA.
AC   Q91HA5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FUSION PROTEIN.
GN   F.
OS   Rinderpest virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11241;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RX   MEDLINE=21014265; PubMed=11186456;
RA   Aianot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RT   "Primary structure of the F-gene from Rinderpest virus strain K.";
RL   Mol. Gen. Mikrobiol. Virusol. 4:29-33(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RA   Ayanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035887; AAK63190.1; -.
SQ   SEQUENCE   546 AA;  58572 MW;  449B2B2DD7405F0B CRC64;


  Query Match             94.1%;  Score 32;  DB 12;  Length 546;
  Best Local Similarity   83.3%;  Pred. No. 66;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIH 6
          ||||:|
Db    435 DRVYLH 440


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds
(without alignments)
3.509 Million cell updates/sec

Title: US-09-723-197-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 26 | 100.0 | 5 | 17 | AAR95670 | Angiotensin II fra |
| 2 | 26 | 100.0 | 5 | 19 | AAW64736 | Angiotensin II pep |
| 3 | 26 | 100.0 | 5 | 19 | AAW65605 | Angiotensin II ana |
| 4 | 26 | 100.0 | 5 | 19 | AAW71118 | Peptide AII(1-5) u |
| 5 | 26 | 100.0 | 5 | 20 | AAY49594 | Angiotensin analog |
| 6 | 26 | 100.0 | 5 | 20 | AAY33909 | Angiotensin II ana |
| 7 | 26 | 100.0 | 5 | 20 | AAY30547 | Amino acid sequenc |
| 8 | 26 | 100.0 | 5 | 20 | AAY30591 | Amino acid sequenc |
| 9 | 26 | 100.0 | 5 | 20 | AAY32722 | Angiotensin II ana |
| 10 | 26 | 100.0 | 5 | 20 | AAY33776 | Angiotensin II (AI |
| 11 | 26 | 100.0 | 5 | 20 | AAY15353 | Angiotensin II (AI |
| 12 | 26 | 100.0 | 5 | 20 | AAY15313 | Angiotensin II (AI |
| 13 | 26 | 100.0 | 5 | 21 | AAB27409 | Angiotensin II ana |
| 14 | 26 | 100.0 | 5 | 21 | AAB28107 | Angiotensin II ana |
| 15 | 26 | 100.0 | 5 | 21 | AAY84568 | Amino acid sequenc |
| 16 | 26 | 100.0 | 5 | 21 | AAY84132 | Peptide comprising |
| 17 | 26 | 100.0 | 5 | 21 | AAY77045 | Angiotensin II (AI |
| 18 | 26 | 100.0 | 5 | 21 | AAY57409 | Angiotensin peptid |
| 19 | 26 | 100.0 | 5 | 22 | AAE08879 | AII peptide (resid |
| 20 | 26 | 100.0 | 5 | 22 | AAE02996 | Human angiotensin |
| 21 | 26 | 100.0 | 5 | 22 | AAE03159 | Human angiotensin |
| 22 | 26 | 100.0 | 5 | 22 | AAB60413 | C-terminally trunc |
| 23 | 26 | 100.0 | 6 | 17 | AAR95669 | Angiotensin II fra |
| 24 | 26 | 100.0 | 6 | 19 | AAW65604 | Angiotensin II ana |
| 25 | 26 | 100.0 | 6 | 19 | AAW64735 | Angiotensin II pep |
| 26 | 26 | 100.0 | 6 | 19 | AAW71117 | Peptide AII(1-6) u |
| 27 | 26 | 100.0 | 6 | 20 | AAY49593 | Angiotensin analog |
| 28 | 26 | 100.0 | 6 | 20 | AAY33908 | Angiotensin II ana |
| 29 | 26 | 100.0 | 6 | 20 | AAY30546 | Amino acid sequenc |
| 30 | 26 | 100.0 | 6 | 20 | AAY30590 | Amino acid sequenc |
| 31 | 26 | 100.0 | 6 | 20 | AAY32721 | Angiotensin II ana |
| 32 | 26 | 100.0 | 6 | 20 | AAY33775 | Angiotensin II (AI |
| 33 | 26 | 100.0 | 6 | 20 | AAY15352 | Angiotensin II (AI |
| 34 | 26 | 100.0 | 6 | 20 | AAY15312 | Angiotensin II (AI |
| 35 | 26 | 100.0 | 6 | 21 | AAB27408 | Angiotensin II ana |
| 36 | 26 | 100.0 | 6 | 21 | AAB28106 | Angiotensin II ana |
| 37 | 26 | 100.0 | 6 | 21 | AAY84131 | Peptide comprising |
| 38 | 26 | 100.0 | 6 | 21 | AAY77044 | Angiotensin II (AI |
| 39 | 26 | 100.0 | 6 | 21 | AAY57408 | Angiotensin peptid |
| 40 | 26 | 100.0 | 6 | 22 | AAE08878 | AII peptide (resid |
| 41 | 26 | 100.0 | 6 | 22 | AAE02995 | Human angiotensin |
| 42 | 26 | 100.0 | 6 | 22 | AAE03158 | Human angiotensin |
| 43 | 26 | 100.0 | 7 | 17 | AAR95665 | Angiotensin II fra |
| 44 | 26 | 100.0 | 7 | 19 | AAW65600 | Angiotensin II ana |
| 45 | 26 | 100.0 | 7 | 19 | AAW64731 | Angiotensin II pep |

ALIGNMENTS

RESULT 1
AAR95670
ID AAR95670 standard; peptide; 5 AA.
XX
AC AAR95670;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(1-5).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 1 drvyi 5

RESULT 2
AAW64736
ID AAW64736 standard; peptide; 5 AA.
XX
AC AAW64736;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #8.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 1 drvyi 5

RESULT 3
AAW65605
ID AAW65605 standard; peptide; 5 AA.
XX
AC AAW65605;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-5).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 4
AAW71118
ID AAW71118 standard; peptide; 5 AA.
XX
AC AAW71118;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-5) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 5
AAY49594
ID AAY49594 standard; peptide; 5 AA.
XX
AC AAY49594;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:9.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5
```

RESULT 6
AAY33909
ID AAY33909 standard; peptide; 5 AA.
XX
AC AAY33909;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-5).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(1-5). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC or AII AT2 type 2 receptor agonists can rapidly provide a large
CC population of ESCs (Embryonic Stem Cell) for use in replacement
CC therapy. Similarly, methods that increase in vivo proliferation of
CC ESCs will enhance the utility of replacement therapy by rapidly
CC increasing local concentration of the stem cells and their progeny at
CC the site of therapy.
CC The method also increases the potential utility of ESCs as vehicles
CC for gene therapy in certain disorders by more efficiently providing
CC a large number of such cells for transfection, and also by providing a
CC more efficient means to rapidly expand transfected ESCs.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5
```

RESULT 7
AAY30547
ID AAY30547 standard; peptide; 5 AA.
XX
AC AAY30547;
XX
DT 18-NOV-1999 (first entry)
XX
DE Amino acid sequence of angiotensin II fragment AII1-5.
XX
KW Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS Synthetic.
XX
PN WO9946285-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05261.
XX
PR 11-MAR-1998; 98US-0077499.
PR 12-JUN-1998; 98US-0089064.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551360/46.
XX
PT An improved method for producing a tissue equivalent with angiotensin I
PT and II derived active agents -
XX
PS Claim 2; Page 56; 83pp; English.
XX
CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes an improved method
CC for producing a tissue equivalent. The method comprises contacting
CC the tissue equivalent with angiotensin I and II derived active
CC agents. The methods are used for production and culture of tissue
CC equivalents (three-dimensional cell and tissue culture systems),
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC vascular graft, cartilage, ligament, collagen lattice, liver and
CC kidney tissue equivalents. The methods and tissue culture systems
CC are used for the long-term proliferation of cells and tissues
CC in an in vitro environment that more closely approximates that found
CC in vivo.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5
```

RESULT 8
AAY30591
ID AAY30591 standard; peptide; 5 AA.
XX
AC AAY30591;
XX
DT 18-NOV-1999 (first entry)
XX
DE Amino acid sequence of an angiotensin II (AII) fragment AII1-5.
XX
KW Angiotensin; analogue; radiation mitigation; tissue damage;
KW radiation therapy; bone marrow transplantation;
KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.
XX
OS Synthetic.
XX
PN WO9945945-A1.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05194.
XX
PR 10-MAR-1998; 98US-0077382.
PR 09-APR-1998; 98US-0081262.
PR 30-APR-1998; 98US-0083670.
PR 19-JUN-1998; 98US-0090096.
PR 22-JUN-1998; 98US-0090216.
PR 11-SEP-1998; 98US-0099957.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA (RODG/) RODGERS K E.
PA (DIZE/) DIZEREGA G.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551209/46.
XX
PT Use of angiotensin and angiotensin type peptides, for mitigating
PT radiation induced tissue damage, improving bone marrow transplantation
PT and promoting megakaryocyte and platelet production -
XX
PS Claim 2; Page 89; 116pp; English.
XX
CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes a method for mitigating
CC radiation induced tissue damage, improving the effectiveness of
CC radiation therapy, to support bone marrow transplantation, and
CC promoting megakaryocyte production and mobilization and platelet
CC production. The method comprises administration of the present peptides.
CC The methods can be used to mitigate radiation induced tissue damage, to
CC improve the effectiveness of radiation therapy, to support bone marrow
CC transplantation, and to promote megakaryocyte production and
CC mobilization and platelet production. They are used particularly in
CC cancer therapy. They can also be used to provide megakaryocytes as
CC vehicles for gene therapy in hematopoietic disorders, by providing a
CC more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 9
AAY32722
ID AAY32722 standard; peptide; 5 AA.
XX
AC AAY32722;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-5).
XX
KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 10
AAY33776
ID AAY33776 standard; peptide; 5 AA.
XX
AC AAY33776;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(1-5).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX

PF 19-FEB-1999; 99WO-US03772.
XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 1 drvyi 5

RESULT 11
AAY15353
ID AAY15353 standard; peptide; 5 AA.
XX
AC AAY15353;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-5).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX
PS Claim 2; Page 10; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 1 drvyi 5

RESULT 12
AAY15313
ID AAY15313 standard; peptide; 5 AA.
XX
AC AAY15313;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-5).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a

```
CC   decapeptide called angiotensin I (AI) which is converted to AII by the
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY15339).
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  13
AAB27409
ID   AAB27409 standard; Peptide; 5 AA.
XX
AC   AAB27409;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Angiotensin II analog AII(1-5).
XX
KW   Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW   cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW   heart valve disease; myocarditis; angiotensin.
XX
OS   Synthetic.
XX
PN   WO200053211-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06198.
XX
PR   09-MAR-1999;   99US-0123678.
PR   31-AUG-1999;   99US-0151874.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-611400/58.
XX
PT   Promoting myocyte proliferation and myocardial tissue repair by
PT   contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT   for treating heart attacks, cardiomyopathies, inflammation and
PT   infection -
XX
PS   Claim 2; Page 10; 55pp; English.
XX
CC   The present invention relates to a method of promoting myocyte
CC   proliferation or differentiation by contacting myocytes with an active
CC   agent containing angiotensinogen, angiotensin I and II  (AI, AII), and
CC   angiotensin analogs. The present sequence is an angiotensin II analog
CC   of the invention. The active agents of the invention may be useful for
CC   promoting myocardial tissue repair following myocardial injury and for
CC   treating heart failure in a mammal. Administration to accelerate in
CC   vivo myocyte proliferation and/or to treat myocardial injuries can be
CC   used to treat cardiomyopathies, inflammation, infection, sepsis,
CC   ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC   ischemia and infarction and for improving cardiac output by increasing
CC   stroke volume.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  14
AAB28107
ID   AAB28107 standard; Peptide; 5 AA.
XX
AC   AAB28107;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Angiotensin II analogue SEQ ID NO: 9.
XX
KW   Wound; scar formation; healing; adhesion formation; AII;
KW   angiotensin II analogue; scar treatment.
XX
OS   Synthetic.
XX
PN   WO200056345-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07669.
XX
PR   23-MAR-1999;   99US-0125707.
PR   16-JUN-1999;   99US-0139541.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-587607/55.
XX
PT   Limiting scar or adhesion formation comprises administering at least
PT   one active agent comprising a peptide -
XX
PS   Claim 2; Page 10; 54pp; English.
XX
CC   The present invention is concerned with peptide analogues of angiotensin
CC   II (AII) which can be used to limit scar and adhesion formation. The
CC   application of AII to wound tissue results in a rapid increase in the
CC   rate of wound healing and causes the proliferation of certain cells, such
CC   as epithelial cells and keratinocytes. Analogues of the protein have been
CC   shown to reduce scar formation, and can be used not only to limit new
CC   scar formation but also to therapeutically treat existing scars. The
CC   wound types include lacerations, burns, punctures, trauma, ulcers,
CC   periodontal conditions, laparotomy and incisional wounds, revision of
CC   hypertrophic scars, genetic hypertrophic scars, keloid scars,
CC   contractures after burns and cosmetic surgical procedures.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  15
AAY84568
ID   AAY84568 standard; Peptide; 5 AA.
XX
AC   AAY84568;
XX
DT   25-JUL-2000  (first entry)
XX
```

DE Amino acid sequence of angiotensin I conversion product Ang(1-5).
XX
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US22976.
XX
PR 30-SEP-1998; 98US-0163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton LS, Robison KE, Hsieh FY;
XX
DR WPI; 2000-293140/25.
XX
PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure -
XX
PS Disclosure; Fig 8; 138pp; English.
XX
CC AAY84563-68 represent angiotensin I conversion products. The
CC specification describes a human angiotensin converting enzyme-2 (ACE-2).
CC ACE-2 is expressed predominantly in kidneys and testis. The sequence of
CC the full length ACE-2 cDNA was determined from a clone obtained from a
CC cDNA library prepared from mRNA of a human heart of a subject who had
CC congestive heart failure. ACE-2 has significant sequence homologies with
CC ACE enzymes, and has also been shown to hydrolyse angiotensin I into
CC Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure
CC related diseases and conditions, such as hypertension, congestive heart
CC failure, chronic heart failure, acute heart failure, myocardial
CC infarction, atherosclerosis and renal failure.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5
```

Search completed: July 1, 2002, 07:41:55
Job time: 347 sec

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-723-197-9
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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 26 | 100.0 | 5 | 2 | US-08-465-775-9 | Sequence 9, Appli |
| 2 | 26 | 100.0 | 5 | 3 | US-09-208-337-9 | Sequence 9, Appli |
| 3 | 26 | 100.0 | 5 | 3 | US-08-990-664-10 | Sequence 10, Appl |
| 4 | 26 | 100.0 | 5 | 4 | US-09-373-962-9 | Sequence 9, Appli |
| 5 | 26 | 100.0 | 5 | 4 | US-09-245-680-9 | Sequence 9, Appli |
| 6 | 26 | 100.0 | 5 | 4 | US-09-198-806C-9 | Sequence 9, Appli |
| 7 | 26 | 100.0 | 5 | 4 | US-09-352-191-9 | Sequence 9, Appli |
| 8 | 26 | 100.0 | 5 | 4 | US-09-012-400-9 | Sequence 9, Appli |
| 9 | 26 | 100.0 | 6 | 2 | US-08-465-775-8 | Sequence 8, Appli |
| 10 | 26 | 100.0 | 6 | 3 | US-09-208-337-8 | Sequence 8, Appli |
| 11 | 26 | 100.0 | 6 | 3 | US-08-990-664-9 | Sequence 9, Appli |
| 12 | 26 | 100.0 | 6 | 4 | US-09-373-962-8 | Sequence 8, Appli |
| 13 | 26 | 100.0 | 6 | 4 | US-09-245-680-8 | Sequence 8, Appli |
| 14 | 26 | 100.0 | 6 | 4 | US-09-198-806C-8 | Sequence 8, Appli |
| 15 | 26 | 100.0 | 6 | 4 | US-09-352-191-8 | Sequence 8, Appli |
| 16 | 26 | 100.0 | 6 | 4 | US-09-012-400-8 | Sequence 8, Appli |
| 17 | 26 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 18 | 26 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 19 | 26 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
| 20 | 26 | 100.0 | 7 | 4 | US-09-373-962-4 | Sequence 4, Appli |
| 21 | 26 | 100.0 | 7 | 4 | US-09-245-680-4 | Sequence 4, Appli |
| 22 | 26 | 100.0 | 7 | 4 | US-09-198-806C-4 | Sequence 4, Appli |
| 23 | 26 | 100.0 | 7 | 4 | US-09-352-191-4 | Sequence 4, Appli |
| 24 | 26 | 100.0 | 7 | 4 | US-09-012-400-4 | Sequence 4, Appli |
| 25 | 26 | 100.0 | 7 | 6 | 5451571-4 | Patent No. 5451571 |
| 26 | 26 | 100.0 | 8 | 1 | US-07-858-842-2 | Sequence 2, Appli |
| 27 | 26 | 100.0 | 8 | 1 | US-08-021-839A-3 | Sequence 3, Appli |
| 28 | 26 | 100.0 | 8 | 1 | US-08-184-935-2 | Sequence 2, Appli |
| 29 | 26 | 100.0 | 8 | 1 | US-08-212-433A-29 | Sequence 29, Appl |
| 30 | 26 | 100.0 | 8 | 1 | US-08-185-448-8 | Sequence 8, Appli |
| 31 | 26 | 100.0 | 8 | 1 | US-07-776-272-1 | Sequence 1, Appli |
| 32 | 26 | 100.0 | 8 | 1 | US-08-428-488-21 | Sequence 21, Appl |
| 33 | 26 | 100.0 | 8 | 1 | US-08-337-781-1 | Sequence 1, Appli |
| 34 | 26 | 100.0 | 8 | 1 | US-08-240-711-20 | Sequence 20, Appl |
| 35 | 26 | 100.0 | 8 | 1 | US-08-594-117-1 | Sequence 1, Appli |
| 36 | 26 | 100.0 | 8 | 1 | US-08-520-770-2 | Sequence 2, Appli |
| 37 | 26 | 100.0 | 8 | 1 | US-08-457-753-20 | Sequence 20, Appl |
| 38 | 26 | 100.0 | 8 | 2 | US-08-115-968-1 | Sequence 1, Appli |
| 39 | 26 | 100.0 | 8 | 2 | US-08-115-968-3 | Sequence 3, Appli |
| 40 | 26 | 100.0 | 8 | 2 | US-08-115-968-4 | Sequence 4, Appli |
| 41 | 26 | 100.0 | 8 | 2 | US-08-465-774-1 | Sequence 1, Appli |
| 42 | 26 | 100.0 | 8 | 2 | US-08-465-774-2 | Sequence 2, Appli |
| 43 | 26 | 100.0 | 8 | 2 | US-08-360-784B-2 | Sequence 2, Appli |
| 44 | 26 | 100.0 | 8 | 2 | US-08-623-833B-4 | Sequence 4, Appli |
| 45 | 26 | 100.0 | 8 | 2 | US-08-465-775-1 | Sequence 1, Appli |

ALIGNMENTS

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RESULT   1
US-08-465-775-9
; Sequence 9, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-9


  Query Match           100.0%;  Score 26;  DB 2;  Length 5;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db       1 DRVYI 5
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US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-9


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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   3
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-10


  Query Match             100.0%;  Score 26;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   4
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-373-962-9


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  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
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US-09-245-680-9
; Sequence 9, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-245-680-9


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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   6
US-09-198-806C-9
; Sequence 9, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-198-806C-9


  Query Match           100.0%;  Score 26;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   7
US-09-352-191-9
; Sequence 9, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-352-191-9


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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   8
US-09-012-400-9
; Sequence 9, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-012-400-9


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          |||||
Db      1 DRVYI 5


RESULT   9
US-08-465-775-8
; Sequence 8, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-8


  Query Match           100.0%;  Score 26;  DB 2;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 DRVYI 5


RESULT  10
US-09-208-337-8
; Sequence 8, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-8


  Query Match           100.0%;  Score 26;  DB 3;  Length 6;
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          |||||
Db      1 DRVYI 5


RESULT  11
US-08-990-664-9
; Sequence 9, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-9


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          |||||
Db      1 DRVYI 5


RESULT 12
US-09-373-962-8
; Sequence 8, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-373-962-8


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          |||||
Db      1 DRVYI 5


RESULT 13
US-09-245-680-8
; Sequence 8, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-245-680-8


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          |||||
Db      1 DRVYI 5


RESULT 14
US-09-198-806C-8
; Sequence 8, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-198-806C-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT 15
US-09-352-191-8
; Sequence 8, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-352-191-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


Search completed: July  1, 2002, 07:43:01
Job time: 302 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:29 ; Search time 69.93 Seconds
(without alignments)
6.870 Million cell updates/sec

Title: US-09-723-197-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 26 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 2 | 26 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 3 | 26 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 4 | 26 | 100.0 | 115 | 2 | A48793 | glycosylation-inhi |
| 5 | 26 | 100.0 | 115 | 2 | I52370 | macrophage migrati |
| 6 | 26 | 100.0 | 115 | 2 | A44499 | macrophage migrati |
| 7 | 26 | 100.0 | 115 | 2 | C47274 | migration inhibito |
| 8 | 26 | 100.0 | 167 | 2 | F83686 | hypothetical prote |
| 9 | 26 | 100.0 | 195 | 1 | B69441 | conserved hypothet |
| 10 | 26 | 100.0 | 238 | 2 | E70337 | ABC transporter - |
| 11 | 26 | 100.0 | 248 | 2 | T44932 | 3-oxoacyl-[acyl-ca |
| 12 | 26 | 100.0 | 312 | 2 | T00992 | hypothetical prote |
| 13 | 26 | 100.0 | 314 | 2 | G97379 | phoE protein U5922 |
| 14 | 26 | 100.0 | 328 | 2 | AF2597 | hypothetical prote |
| 15 | 26 | 100.0 | 396 | 2 | AD0310 | hypothetical prote |
| 16 | 26 | 100.0 | 409 | 1 | G69000 | molybdenum cofacto |
| 17 | 26 | 100.0 | 476 | 1 | JC2318 | angiotensin precur |
| 18 | 26 | 100.0 | 477 | 1 | ANRT | angiotensin precur |
| 19 | 26 | 100.0 | 477 | 1 | A29978 | angiotensin precur |
| 20 | 26 | 100.0 | 485 | 1 | ANHU | angiotensin precur |
| 21 | 26 | 100.0 | 509 | 2 | T06300 | hypothetical prote |
| 22 | 26 | 100.0 | 518 | 2 | B64449 | 2-isopropylmalate |
| 23 | 26 | 100.0 | 540 | 2 | S72233 | transcription fact |
| 24 | 26 | 100.0 | 575 | 1 | HNNZSZ | hemagglutinin-neur |
| 25 | 26 | 100.0 | 575 | 1 | HNNZSH | hemagglutinin-neur |
| 26 | 26 | 100.0 | 575 | 2 | S12135 | hemagglutinin-neur |
| 27 | 26 | 100.0 | 576 | 1 | HNNZS | hemagglutinin-neur |
| 28 | 26 | 100.0 | 581 | 1 | A37913 | serine/threonine-s |
| 29 | 26 | 100.0 | 584 | 2 | A97171 | uncharacterized pr |
| 30 | 26 | 100.0 | 614 | 2 | T43121 | hypothetical prote |
| 31 | 26 | 100.0 | 644 | 2 | G64938 | hypothetical prote |
| 32 | 26 | 100.0 | 644 | 2 | F82145 | conserved hypothet |
| 33 | 26 | 100.0 | 644 | 2 | D90940 | hypothetical prote |
| 34 | 26 | 100.0 | 644 | 2 | H85788 | hypothetical prote |
| 35 | 26 | 100.0 | 644 | 2 | AF0262 | conserved hypothet |
| 36 | 26 | 100.0 | 644 | 2 | AD0712 | conserved hypothet |
| 37 | 26 | 100.0 | 661 | 2 | C83843 | hypothetical prote |
| 38 | 26 | 100.0 | 676 | 1 | WMBEX6 | UL6 protein - huma |
| 39 | 26 | 100.0 | 688 | 2 | A44306 | polyphosphate kina |
| 40 | 26 | 100.0 | 688 | 2 | C91049 | polyphosphate kina |
| 41 | 26 | 100.0 | 688 | 2 | G85893 | polyphosphate kina |
| 42 | 26 | 100.0 | 688 | 2 | AC0819 | polyphosphate kina |
| 43 | 26 | 100.0 | 739 | 2 | I40715 | malate synthase (E |
| 44 | 26 | 100.0 | 749 | 2 | S77175 | sensory transducti |
| 45 | 26 | 100.0 | 778 | 2 | T44761 | probable preprotei |

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 26; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
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RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 26; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
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RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 DRVYI 5

RESULT 4
A48793
glycosylation-inhibiting factor - human
N;Alternate names: macrophage migration inhibitory 12.7K protein; sarcolectin
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: A48793; A49612; A33838; A47274; S34300; S33277
R;Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A;Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A;Reference number: A48793; MUID:94052102
A;Accession: A48793
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <MIK>
A;Cross-references: GB:L10612; NID:g402701; PIDN:AAA35892.1; PID:g402702
R;Paralkar, V.; Wistow, G.
Genomics 19, 48-51, 1994
A;Title: Cloning the human gene for macrophage migration inhibitory factor (MIF).
A;Reference number: A49612; MUID:94245178
A;Accession: A49612
A;Molecule type: DNA
A;Residues: 1-115 <PAR>
A;Cross-references: GB:L19686; NID:g307284; PIDN:AAA21814.1; PID:g307285
R;Weiser, W.Y.; Temple, P.A.; Witek-Giannotti, J.S.; Remold, H.G.; Clark, S.C.; David, J
Proc. Natl. Acad. Sci. U.S.A. 86, 7522-7526, 1989
A;Title: Molecular cloning of a cDNA encoding a human macrophage migration inhibitory fa
A;Reference number: A33838; MUID:90017510
A;Accession: A33838
A;Molecule type: mRNA
A;Residues: 1-105,'S',107-115 <WEI>
A;Cross-references: GB:M25639; NID:g188555; PIDN:AAA36315.1; PID:g188556
A;Experimental source: activated T cells
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A;Reference number: A47274; MUID:93165679
A;Accession: A47274
A;Molecule type: mRNA
A;Residues: 10-115 <WIS>
A;Cross-references: GB:M95775; NID:g187180; PIDN:AAA36179.1; PID:g187181
A;Experimental source: fetal lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124868, NCBIP:124871)

R;Bucala, R.; Mitchell, R.A.; Bernhagen, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34300
A;Accession: S34300
A;Molecule type: mRNA
A;Residues: 1-115 <BUC>
A;Cross-references: EMBL:Z23063; NID:g312333; PIDN:CAA80598.1; PID:g312334
R;Zeng, F.Y.; Weiser, W.Y.; Kratzin, H.; Stahl, B.; Karas, M.; Gabius, H.J.
Arch. Biochem. Biophys. 303, 74-80, 1993
A;Title: The major binding protein of the interferon antagonist sarcolectin in human
A;Reference number: S33277; MUID:93256574
A;Accession: S33277
A;Molecule type: protein
A;Residues: 3-24 <ZEN>
A;Experimental source: placenta
A;Note: there is no signal sequence; the mature protein starts with residue 3
C;Genetics:
A;Gene: GDB:MIF
A;Cross-references: GDB:138402; OMIM:153620
A;Map position: 22q11.2-22q11.2
A;Introns: 36/3; 94/2
A;Note: appears to be a single copy gene (see reference A49612)
C;Superfamily: bovine glycosylation-inhibiting factor
F;3-115/Product: macrophage migration inhibitory factor #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
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Db 93 DRVYI 97

RESULT 5
I52370
macrophage migration inhibitory factor MIF [similarity] - rat
C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I52370
R;Sakai, M.; Nishihira, J.; Hibiya, Y.; Koyama, Y.; Nishi, S.
Biochem. Mol. Biol. Int. 33, 439-446, 1994
A;Title: Glutathione binding rat liver 13k protein is the homologue of the macrophage
A;Reference number: I52370; MUID:95038523
A;Accession: I52370
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: GB:S73424; NID:g663139; PIDN:AAB32392.1; PID:g663140
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 93 DRVYI 97

RESULT 6
A44499
macrophage migration inhibitory factor DER6 - mouse
N;Alternate names: glycosylation-inhibiting factor; migration inhibitory factor, 10K
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A44499; S34299; B47274; I49691; S38325; I56259
R;Lanahan, A.; Williams, J.B.; Sanders, L.K.; Nathans, D.
Mol. Cell. Biol. 12, 3919-3929, 1992
A;Title: Growth factor-induced delayed early response genes.
A;Reference number: A44499; MUID:92375060

A;Accession: A44499
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <LAN>
A;Experimental source: BALB/c 3T3 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:111643)
R;Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.; Tracey, K.J.; Manogue, K.; Vo
submitted to the EMBL Data Library, June 1993
A;Reference number: S34299
A;Accession: S34299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <BER>
A;Cross-references: EMBL:Z23048; NID:g312220; PIDN:CAA80583.1; PID:g312221
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A;Reference number: A47274; MUID:93165679
A;Accession: B47274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 6-115 <WIS>
A;Cross-references: GB:L07607; NID:g191490; PIDN:AAA37111.1; PID:g191491
A;Experimental source: lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124869, NCBIP:124872)
R;Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A;Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A;Reference number: A48793; MUID:94052102
A;Accession: I49691
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: GB:L10613; NID:g402716; PIDN:AAA37693.1; PID:g402717
R;Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.B.; Tracey, K.J.; Voelter, W.;
Nature 365, 756-759, 1993
A;Title: MIF is a pituitary-derived cytokine that potentiates lethal endotoxaemia.
A;Reference number: S38325; MUID:94019845
A;Accession: S38325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 2-28 <BE2>
A;Cross-references: EMBL:Z23048
R;Mitchell, R.; Bacher, M.; Bernhagen, J.; Pushkarskaya, T.; Seldin, M.F.; Bucala, R.
J. Immunol. 154, 3863-3870, 1995
A;Title: Cloning and characterization of the gene for mouse macrophage migration inhibit
A;Reference number: I56259; MUID:95221891
A;Accession: I56259
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <RE2>
A;Cross-references: GB:L39357; NID:g790847; PIDN:AAA74321.1; PID:g790848
C;Genetics:
A;Gene: Mif
A;Introns: 36/3; 94/2
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 93 DRVYI 97

RESULT 7
C47274
migration inhibitory factor, 10K - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: C47274
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating
A;Reference number: A47274; MUID:93165679
A;Accession: C47274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-115 <WIS>
A;Cross-references: GB:M95776; NID:g212257; PIDN:AAA48939.1; PID:g212258
A;Experimental source: embryo, lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124870, NCBIP:124873)
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 93 DRVYI 97

RESULT 8
F83686
hypothetical protein BH0294 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83686
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83686
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04013.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0294

Query Match 100.0%; Score 26; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| 
Db 61 DRVYI 65

RESULT 9
B69441
conserved hypothetical protein AF1531 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: B69441
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343
A;Accession: B69441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <KLE>
A;Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89717.1; PID:g264
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0038

Query Match 100.0%; Score 26; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
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Db     68 DRVYI 72
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RESULT 10
E70337
ABC transporter - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Feb-2001
C;Accession: E70337
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: E70337
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <AQF>
A;Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06695.1; PID:g2983089; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: abcT7
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;17-210/Domain: ATP-binding cassette homology <ABC>
F;34-41/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 26; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
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Db    202 DRVYI 206
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RESULT 11
T44932
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Agrobacterium tum
C;Species: Agrobacterium tumefaciens
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44932
R;Kim, K.S.; Farrand, S.K.
J. Bacteriol. 178, 3275-3284, 1996
A;Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mar
by the plant tumor.
A;Reference number: Z22872; MUID:96236046
A;Accession: T44932
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-248 <KIM>
A;Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07783.1; PID:g797334
A;Experimental source: strain 15955
C;Genetics:
A;Gene: mocC
A;Genome: plasmid pTi15955
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase

Query Match 100.0%; Score 26; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
          |||||
Db    221 DRVYI 225
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RESULT 12
T00992
hypothetical protein At2g26590 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T9J22.26
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00992; D84662
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, April 1998
A;Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
A;Reference number: Z14161
A;Accession: T00992
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <ROU>
A;Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739383
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <STO>
A;Cross-references: GB:AE002093; NID:g2739383; PIDN:AAC14506.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g26590; T9J22.26
A;Map position: 2
A;Introns: 11/3; 42/3; 62/3; 100/3; 124/2; 169/2; 210/1; 241/3; 267/3; 286/1

Query Match 100.0%; Score 26; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
          |||||
Db     81 DRVYI 85
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RESULT 13
G97379
phoE protein U59229 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: G97379
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
A;Accession: G97379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK85992.1; PID:g15155055; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_285
A;Map position: circular chromosome

Query Match 100.0%; Score 26; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
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          |||||
Db     94 DRVYI 98


RESULT  14
AF2597
hypothetical protein phnE [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AF2597
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AF2597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41196.1; PID:g17738497; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: phnE
A;Map position: circular chromosome


  Query Match             100.0%;  Score 26;  DB 2;  Length 328;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     108 DRVYI 112


RESULT  15
AD0310
hypothetical protein YPO2542 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0310
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC91344.1; PID:g15980533; GSPDB:GN00175
C;Genetics:
A;Gene: YPO2542


  Query Match             100.0%;  Score 26;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     19 DRVYI 23



Search completed: July  1, 2002, 07:46:30
Job time: 451 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:09 ; Search time 34.05 Seconds
(without alignments)
5.686 Million cell updates/sec

Title: US-09-723-197-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 26 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 26 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 3 | 26 | 100.0 | 114 | 1 | MIF_CHICK | Q02960 gallus gall |
| 4 | 26 | 100.0 | 114 | 1 | MIF_HUMAN | P14174 homo sapien |
| 5 | 26 | 100.0 | 114 | 1 | MIF_MOUSE | P34884 mus musculu |
| 6 | 26 | 100.0 | 114 | 1 | MIF_RAT | P30904 rattus norv |
| 7 | 26 | 100.0 | 436 | 1 | TBX6_HUMAN | O95947 homo sapien |
| 8 | 26 | 100.0 | 476 | 1 | ANGT_SHEEP | P20757 ovis aries |
| 9 | 26 | 100.0 | 477 | 1 | ANGT_MOUSE | P11859 mus musculu |
| 10 | 26 | 100.0 | 477 | 1 | ANGT_RAT | P01015 rattus norv |
| 11 | 26 | 100.0 | 485 | 1 | ANGT_HUMAN | P01019 homo sapien |
| 12 | 26 | 100.0 | 518 | 1 | YB95_METJA | Q58595 methanococc |
| 13 | 26 | 100.0 | 540 | 1 | TBX6_MOUSE | P70327 mus musculu |
| 14 | 26 | 100.0 | 575 | 1 | HEMA_SEND5 | P27562 sendai viru |
| 15 | 26 | 100.0 | 575 | 1 | HEMA_SENDF | P19758 sendai viru |
| 16 | 26 | 100.0 | 575 | 1 | HEMA_SENDJ | P06863 sendai viru |
| 17 | 26 | 100.0 | 575 | 1 | HEMA_SENDZ | P04853 sendai viru |
| 18 | 26 | 100.0 | 576 | 1 | HEMA_SENDH | P03425 sendai viru |
| 19 | 26 | 100.0 | 581 | 1 | MIK1_SCHPO | P30290 schizosacch |
| 20 | 26 | 100.0 | 644 | 1 | YEAG_ECOLI | P77391 escherichia |
| 21 | 26 | 100.0 | 676 | 1 | UL06_HSV11 | P10190 herpes simp |
| 22 | 26 | 100.0 | 687 | 1 | PPK_ECOLI | P28688 escherichia |
| 23 | 26 | 100.0 | 687 | 1 | PPK_SALTY | O86090 salmonella |
| 24 | 26 | 100.0 | 738 | 1 | MASZ_CORGL | P42450 corynebacte |
| 25 | 26 | 100.0 | 778 | 1 | SEA2_MYCLE | O32922 mycobacteri |
| 26 | 26 | 100.0 | 808 | 1 | SEA2_MYCTU | Q50612 mycobacteri |
| 27 | 26 | 100.0 | 1071 | 1 | CARB_BACSU | P25994 bacillus su |
| 28 | 26 | 100.0 | 1295 | 1 | BXA1_CLOBO | P10845 clostridium |
| 29 | 26 | 100.0 | 1295 | 1 | BXA2_CLOBO | Q45894 clostridium |
| 30 | 26 | 100.0 | 2061 | 1 | MYOF_HUMAN | Q9nzm1 homo sapien |
| 31 | 25 | 96.2 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 32 | 25 | 96.2 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 33 | 25 | 96.2 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 34 | 25 | 96.2 | 114 | 1 | MIF_BOVIN | P80177 bos taurus |
| 35 | 25 | 96.2 | 114 | 1 | MIF_MERUN | O55052 meriones un |
| 36 | 25 | 96.2 | 178 | 1 | BDH_BOVIN | Q02337 bos taurus |
| 37 | 25 | 96.2 | 272 | 1 | PK1_NPVAC | P41415 autographa |
| 38 | 25 | 96.2 | 311 | 1 | NFE2_RHIME | Q52994 rhizobium m |
| 39 | 25 | 96.2 | 446 | 1 | GGAA_BACSU | P46917 bacillus su |
| 40 | 25 | 96.2 | 465 | 1 | YC14_KLEPN | Q48460 klebsiella |
| 41 | 25 | 96.2 | 488 | 1 | GAL7_LACHE | Q00054 lactobacill |
| 42 | 25 | 96.2 | 511 | 1 | EGO_ECOLI | P77257 escherichia |
| 43 | 25 | 96.2 | 539 | 1 | PRIS_METJA | Q58175 methanococc |
| 44 | 25 | 96.2 | 572 | 1 | HEMA_PI3B | P06167 bovine para |
| 45 | 25 | 96.2 | 574 | 1 | CDAS_THEET | P29964 thermoanaer |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 26; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 DRVYI 5

RESULT 2
ANGT_HORSE
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";

```
RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   3
MIF_CHICK
ID   MIF_CHICK      STANDARD;      PRT;   114 AA.
AC   Q02960;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase).
GN   MIF.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; M95776; AAA48939.1; -.
DR   PIR; C47274; C47274.
DR   HSSP; P34884; 1MFI.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine.
FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
FT   INIT_MET      0      0       BY SIMILARITY.
SQ   SEQUENCE   114 AA;  12353 MW;  A55222D00E6D05CF CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     92 DRVYI 96


RESULT   4
MIF_HUMAN
ID   MIF_HUMAN      STANDARD;      PRT;   114 AA.
AC   P14174;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Glycosylation-inhibiting factor) (GIF).
GN   MIF OR MMIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90017510; PubMed=2552447;
RA   Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,
RA   Clark S.C., David J.R.;
RT   "Molecular cloning of a cDNA encoding a human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245178; PubMed=8188240;
RA   Paralkar V., Wistow G.J.;
RT   "Cloning the human gene for macrophage migration inhibitory factor
RT   (MIF).";
RL   Genomics 19:48-51(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,
RA   Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE OF 9-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [5]
RP   SEQUENCE OF 1-10.
RC   TISSUE=Liver;
RX   MEDLINE=93162045; PubMed=1286669;
RA   Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA   Appel R.D., Hughes G.J.;
RT   "Human liver protein map: a reference database established by
RT   microsequencing and gel comparison.";
RL   Electrophoresis 13:992-1001(1992).
RN   [6]
RP   SEQUENCE OF 2-23.
RX   MEDLINE=93256574; PubMed=7683862;
RA   Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gabius H.J.;
RT   "The major binding protein of the interferon antagonist sarcolectin
```

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RT   in human placenta is a macrophage migration inhibitory factor.";
RL   Arch. Biochem. Biophys. 303:74-80(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=96338096; PubMed=8766818;
RA   Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;
RT   "Crystal structure of macrophage migration inhibitory factor from
RT   human lymphocyte at 2.1-A resolution.";
RL   FEBS Lett. 389:145-148(1996).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=96181524; PubMed=8610159;
RA   Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Mikayama T.,
RA   Ishizaka K., Kuroki R.;
RT   "The crystal structure of human glycosylation-inhibiting factor is a
RT   trimeric barrel with three 6-stranded beta-sheets.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=96224258; PubMed=8643551;
RA   Sun H.W., Bernhagen J., Bucala R., Lolis E.;
RT   "Crystal structure at 2.6-A resolution of human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=99282199; PubMed=10353846;
RA   Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;
RT   "Pro-1 of macrophage migration inhibitory factor functions as a
RT   catalytic base in the phenylpyruvate tautomerase activity.";
RL   Biochemistry 38:7346-7354(1999).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE
CC       SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA
CC       OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF
CC       CHRONIC INFLAMMATORY LOCI.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z23063; CAA80598.1; -.
DR   EMBL; M25639; AAA36315.1; -.
DR   EMBL; M95775; AAA36179.1; -.
DR   EMBL; L10612; AAA35892.1; -.
DR   EMBL; L19686; AAA21814.1; -.
DR   PIR; A33838; A33838.
DR   PIR; S33277; S33277.
DR   PDB; 1GIF; 12-MAR-97.
DR   PDB; 1MIF; 07-DEC-96.
DR   PDB; 1P1G; 07-JUN-99.
DR   PDB; 1CGQ; 07-JUN-99.
DR   PDB; 1CA7; 30-JUN-99.
DR   SWISS-2DPAGE; P14174; HUMAN.
DR   Siena-2DPAGE; P14174; -.
DR   MIM; 153620; -.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
FT   CONFLICT    105    105       N -> S (IN REF. 1).
SQ   SEQUENCE   114 AA;  12345 MW;  4BD525232B3F3069 CRC64;
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  Query Match           100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      92 DRVYI 96


RESULT   5
MIF_MOUSE
ID   MIF_MOUSE      STANDARD;      PRT;   114 AA.
AC   P34884;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Delayed early response protein 6) (DER6) (Glycosylation-
DE   inhibiting factor).
GN   MIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC   TISSUE=Pituitary;
RX   MEDLINE=94019845; PubMed=8413654;
RA   Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,
RA   Tracey K.J., Voelter W., Manogue K.R., Cerami A., Bucala R.;
RT   "MIF is a pituitary-derived cytokine that potentiates lethal
RT   endotoxaemia.";
RL   Nature 365:756-759(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=92375060; PubMed=1508193;
RA   Lanahan A., Williams J.B., Sanders L.K., Nathans D.;
RT   "Growth factor-induced delayed early response genes.";
RL   Mol. Cell. Biol. 12:3919-3929(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,
RA   Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=95221891; PubMed=7706726;
RA   Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,
RA   Bucala R.;
RT   "Cloning and characterization of the gene for mouse macrophage
RT   migration inhibitory factor (MIF).";
RL   J. Immunol. 154:3863-3870(1995).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047325; PubMed=7558021;
RA   Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,
RA   Copeland N.G., David J.R., Gerard C.;
RT   "Structural characterization and chromosomal location of the mouse
RT   macrophage migration inhibitory factor gene and pseudogenes.";
RL   Genomics 27:412-419(1995).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047324; PubMed=7558020;
RA   Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,
RA   Wistow G.;
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RT   "Genomic cloning of mouse MIF (macrophage inhibitory factor) and
RT   genetic mapping of the human and mouse expressed gene and nine mouse
RT   pseudogenes.";
RL   Genomics 27:405-411(1995).
RN   [7]
RP   SEQUENCE OF 5-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX   MEDLINE=99303983; PubMed=10360941;
RA   Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L.,
RA   Whitman C.P.;
RT   "Crystal structure of macrophage migration inhibitory factor
RT   complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution:
RT   implications for enzymatic catalysis and inhibition.";
RL   Biochemistry 38:7444-7452(1999).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).
RX   MEDLINE=20393856; PubMed=10933783;
RA   Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;
RT   "Mechanism of the phenylpyruvate tautomerase activity of macrophage
RT   migration inhibitory factor: properties of the P1G, P1A, Y95F, and
RT   N97A mutants.";
RL   Biochemistry 39:9671-9678(2000).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23048; CAA80583.1; -.
DR   EMBL; U19825; AAA91637.1; -.
DR   EMBL; L10613; AAA37693.1; -.
DR   EMBL; U20156; AAA91638.1; -.
DR   EMBL; L39357; AAA74321.1; -.
DR   EMBL; L07607; AAA37111.1; -.
DR   PIR; S34299; S34299.
DR   PIR; A44499; A44499.
DR   PDB; 1MFF; 11-AUG-00.
DR   PDB; 1MFI; 22-JUN-99.
DR   MGD; MGI:96982; Mif.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
SQ   SEQUENCE   114 AA;  12373 MW;  8FD2339CF0792F9E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     92 DRVYI 96


RESULT   6
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MIF_RAT
ID   MIF_RAT        STANDARD;      PRT;   114 AA.
AC   P30904;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Glutathione-binding 13 kDa protein).
GN   MIF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95038523; PubMed=7951062;
RA   Sakai M., Nishihira J., Hibiya Y., Koyama Y., Nishi S.;
RT   "Glutathione binding rat liver 13k protein is the homologue of the
RT   macrophage migration inhibitory factor.";
RL   Biochem. Mol. Biol. Int. 33:439-446(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RA   Wen Y., Li G., Bekhor I.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PVG/C;
RA   Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B.,
RA   Reynolds A.J., Whitehouse C.J.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-25.
RX   MEDLINE=93063370; PubMed=1436109;
RA   Blocki F.A., Schlievert P.M., Wackett L.P.;
RT   "Rat liver protein linking chemical and immunological detoxification
RT   systems.";
RL   Nature 360:269-270(1992).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC   TISSUE=Liver;
RX   MEDLINE=96186248; PubMed=8605628;
RA   Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J.,
RA   Sakai M.;
RT   "Crystal structure of the macrophage migration inhibitory factor from
RT   rat liver.";
RL   Nat. Struct. Biol. 3:259-266(1996).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS
CC       INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S73424; AAB32392.1; -.
DR   EMBL; U20999; AAA62644.1; -.
DR   EMBL; U62326; AAB04024.1; -.
DR   PDB; 1FIM; 11-JUL-96.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
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FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
FT   CONFLICT     50     50       S -> R (IN REF. 2).
SQ   SEQUENCE   114 AA;  12346 MW;  9E33C39CF064329E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      92 DRVYI 96


RESULT   7
TBX6_HUMAN
ID   TBX6_HUMAN      STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
RN   [2]
RP   SEQUENCE OF 135-272 FROM N.A.
RC   TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     170 DRVYI 174


RESULT   8
ANGT_SHEEP
ID   ANGT_SHEEP      STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    476       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
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FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      25 DRVYI 29


RESULT   9
ANGT_MOUSE
ID   ANGT_MOUSE     STANDARD;      PRT;   477 AA.
AC   P11859;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88284703; PubMed=3397061;
RA   Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT   "Molecular cloning of the mouse angiotensinogen gene.";
RL   Genomics 2:240-248(1988).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF045887; AAC01765.1; -.
DR   EMBL; AF045886; AAC01765.1; JOINED.
DR   EMBL; AF045885; AAC01765.1; JOINED.
DR   EMBL; AF045884; AAC01765.1; JOINED.
DR   PIR; A29978; A29978.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51990 MW;  A877F4029F338607 CRC64;
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  Query Match             100.0%;  Score 26;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      25 DRVYI 29


RESULT  10
ANGT_RAT
ID   ANGT_RAT       STANDARD;      PRT;   477 AA.
AC   P01015;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR;
RX   MEDLINE=83169849; PubMed=6572971;
RA   Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA   Nakanishi S.;
RT   "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN   [2]
RP   SEQUENCE OF 25-34.
RX   MEDLINE=73060322; PubMed=4344907;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. II. Structure of rat
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 20:1579-1581(1972).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L00094; AAA98779.1; -.
DR   EMBL; L00091; AAA98779.1; JOINED.
DR   EMBL; L00092; AAA98779.1; JOINED.
DR   EMBL; L00093; AAA98779.1; JOINED.
DR   PIR; A01251; ANRT.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51981 MW;  689051A5788D693D CRC64;
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  Query Match             100.0%;  Score 26;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      25 DRVYI 29


RESULT  11
ANGT_HUMAN
ID   ANGT_HUMAN     STANDARD;      PRT;   485 AA.
AC   P01019; Q16358; Q16359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89170129; PubMed=2924688;
RA   Gaillard I., Clauser E., Corvol P.;
RT   "Structure of human angiotensinogen gene.";
RL   DNA 8:87-99(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85000455; PubMed=6089875;
RA   Kageyama R., Ohkubo H., Nakanishi S.;
RT   "Primary structure of human preangiotensinogen deduced from the
RT   cloned cDNA sequence.";
RL   Biochemistry 23:3603-3609(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90237063; PubMed=1692023;
RA   Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA   Murakami K.;
RT   "Structure and expression of the human angiotensinogen gene.
RT   Identification of a unique and highly active promoter.";
RL   J. Biol. Chem. 265:7576-7582(1990).
RN   [4]
RP   SEQUENCE OF 1-338 FROM N.A.
RX   MEDLINE=87244745; PubMed=2885106;
RA   Kunapuli S.P., Kumar A.;
RT   "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT   presence of its mRNA in rat heart.";
RL   Circ. Res. 60:786-790(1987).
RN   [5]
RP   SEQUENCE OF 34-45, AND SUBUNITS.
RC   TISSUE=Serum;
RX   MEDLINE=95293954; PubMed=7539791;
RA   Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA   Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT   "Identification of angiotensinogen and complement C3dg as novel
RT   proteins binding the proform of eosinophil major basic protein in
RT   human pregnancy serum and plasma.";
RL   J. Biol. Chem. 270:13645-13651(1995).
RN   [6]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=69014170; PubMed=4300938;
RA   Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT   "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL   Biochim. Biophys. Acta 168:106-112(1968).
RN   [7]
RP   STRUCTURE BY NMR OF ANGIOTENSIN II.
RX   MEDLINE=98151281; PubMed=9492317;
RA   Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT   "The octapeptide angiotensin II adopts a well-defined structure in a
RT   phospholipid environment.";
RL   Eur. J. Biochem. 251:448-453(1998).
RN   [8]
RP   VARIANTS MET-207; THR-268 AND CYS-281.
RX   MEDLINE=93008239; PubMed=1394429;
RA   Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA   Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA   Lalouel J.-M., Corvol P.;
RT   "Molecular basis of human hypertension: role of angiotensinogen.";
RL   Cell 71:169-180(1992).
RN   [9]
RP   VARIANT THR-268.
RX   MEDLINE=93291876; PubMed=8513325;
RA   Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA   Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
RA   Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT   "A molecular variant of angiotensinogen associated with
RT   preeclampsia.";
RL   Nat. Genet. 4:59-61(1993).
RN   [10]
RP   VARIANTS ILE-242; ARG-244 AND CYS-281.
RX   MEDLINE=95331754; PubMed=7607642;
RA   Hixson J.E., Powers P.K.;
RT   "Detection and characterization of new mutations in the human
RT   angiotensinogen gene (AGT).";
RL   Hum. Genet. 96:110-112(1995).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
CC       heterotetramer with the proform of PRG2 and as a complex (probably
CC       a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
CC       ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
CC       (PIH) (PREECLAMPSIA).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02215; AAA51731.1; -.
DR   EMBL; M24689; AAA51679.1; -.
DR   EMBL; M24686; AAA51679.1; JOINED.
DR   EMBL; M24687; AAA51679.1; JOINED.
DR   EMBL; M24688; AAA51679.1; JOINED.
DR   EMBL; X15324; CAA33385.1; -.
DR   EMBL; X15325; CAA33385.1; JOINED.
DR   EMBL; X15326; CAA33385.1; JOINED.
DR   EMBL; X15327; CAA33385.1; JOINED.
DR   EMBL; M69110; AAA52282.1; -.
DR   EMBL; S78529; AAD14287.1; -.
DR   EMBL; S78530; AAD14288.1; -.
DR   PIR; A01249; ANHU.
DR   PIR; A31362; A31362.
DR   PIR; A35203; A35203.
DR   SWISS-2DPAGE; P01019; HUMAN.
DR   MIM; 106150; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
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KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW   Disease mutation; Polymorphism.
FT   SIGNAL        1     33
FT   CHAIN        34    485       ANGIOTENSINOGEN.
FT   PEPTIDE      34     43       ANGIOTENSIN I.
FT   PEPTIDE      34     41       ANGIOTENSIN II.
FT   CARBOHYD     47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     207    207       T -> M.
FT                                /FTId=VAR_007093.
FT   VARIANT     242    242       T -> I (IN HYPERTENSION).
FT                                /FTId=VAR_007094.
FT   VARIANT     244    244       L -> R (IN HYPERTENSION).
FT                                /FTId=VAR_007095.
FT   VARIANT     268    268       M -> T (IN HYPERTENSION).
FT                                /FTId=VAR_007096.
FT   VARIANT     281    281       Y -> C (IN HYPERTENSION).
FT                                /FTId=VAR_007097.
FT   CONFLICT    333    333       Q -> E (IN REF. 1).
SQ   SEQUENCE   485 AA;  53154 MW;  5026C2DFB2DD236E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     34 DRVYI 38


RESULT  12
YB95_METJA
ID   YB95_METJA     STANDARD;      PRT;   518 AA.
AC   Q58595;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative 2-isopropylmalate/homocitrate synthase MJ1195 (EC 4.1.3.-).
GN   MJ1195.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE
CC       SYNTHASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67561; AAB99199.1; -.
DR   TIGR; MJ1195; -.
DR   InterPro; IPR002034; AIPM_homocit_synth.
DR   InterPro; IPR000891; HMGL-like.
DR   Pfam; PF00682; HMGL-like; 1.
DR   PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR   PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
KW   Hypothetical protein; Lyase; Complete proteome.
SQ   SEQUENCE   518 AA;  56620 MW;  604AB61B41E607A4 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 518;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     22 DRVYI 26


RESULT  13
TBX6_MOUSE
ID   TBX6_MOUSE     STANDARD;      PRT;   540 AA.
AC   P70327;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97032942; PubMed=8878690;
RA   Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA   Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT   "Evolution of mouse T-box genes by tandem duplication and cluster
RT   dispersion.";
RL   Genetics 144:249-254(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastrula;
RX   MEDLINE=97115702; PubMed=8954725;
RA   Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT   "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT   gastrulation.";
RL   Dev. Biol. 180:534-542(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=98140705; PubMed=9490412;
RA   Chapman D.L., Papaioannou V.E.;
RT   "Three neural tubes in mouse embryos with mutations in the T-box gene
RT   Tbx6.";
RL   Nature 391:695-697(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC       MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC       DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC       PATHWAY.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC       STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC       MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC       PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC       AS THE SOURCE OF MESODERM.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U57331; AAC53110.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:102539; Tbx6.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       61     64       POLY-ALA.
FT   DOMAIN       79     82       POLY-PRO.
FT   DNA_BIND    100    273       T-BOX.
SQ   SEQUENCE   540 AA;  58628 MW;  BC834CE2745E8E61 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    170 DRVYI 174


RESULT  14
HEMA_SEND5
ID   HEMA_SEND5     STANDARD;      PRT;   575 AA.
AC   P27562;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN   HN.
OS   Sendai virus (strain Z / host mutants).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX   NCBI_TaxID=11192;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUTANT TS-F1, AND MUTANT F1-R;
RX   MEDLINE=90266486; PubMed=2161155;
RA   Middleton Y., Tashiro M., Thai T., Oh J., Seymour J., Pritzer E.,
RA   Klenk H.D., Rott R., Seto J.T.;
RT   "Nucleotide sequence analyses of the genes encoding the HN, M, NP, P,
RT   and L proteins of two host range mutants of Sendai virus.";
RL   Virology 176:656-657(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUTANT F1-R / T-5 REVERTANT;
RX   MEDLINE=91335752; PubMed=1651590;
RA   Tashiro M., James I., Karri S., Wahn K., Tobita K., Klenk H.D.,
RA   Rott R., Seto J.T.;
RT   "Pneumotropic revertants derived from a pantropic mutant, F1-R, of
RT   Sendai virus.";
RL   Virology 184:227-234(1991).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC       TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC       ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC       THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC       GLYCOPROTEINS.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC       alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC       oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC       synthetic substrates.
CC   -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC       N-TERMINAL HYDROPHOBIC SEQUENCE.
CC   -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC       NEURAMINIDASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M30202; AAB06282.1; -.
DR   EMBL; M30203; AAB06288.1; -.
DR   EMBL; M30204; AAB06200.1; -.
DR   EMBL; M69046; AAB06294.1; -.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;
KW   Transmembrane.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     60       POTENTIAL.
FT   DOMAIN       61    575       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    511    511       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   575 AA;  63469 MW;  86EE95B73AD7EB2D CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 575;
  Best Local Similarity   100.0%;  Pred. No. 70;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    419 DRVYI 423


RESULT  15
HEMA_SENDF
ID   HEMA_SENDF     STANDARD;      PRT;   575 AA.
AC   P19758;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN   HN.
OS   Sendai virus (strain Fushimi).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX   NCBI_TaxID=11195;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91057133; PubMed=2173829;
RA   Neubert W.J., Willenbrink W.;
RT   "Cloning and sequencing of the HN gene of Sendai virus (strain
RT   Fushimi).";
RL   Nucleic Acids Res. 18:6427-6427(1990).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC       TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC       ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC       THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC       GLYCOPROTEINS.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC       alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC       oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC       synthetic substrates.
CC   -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC       N-TERMINAL HYDROPHOBIC SEQUENCE.
CC   -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC       NEURAMINIDASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X56131; CAA39596.1; -.
DR   PIR; S12135; S12135.
DR   PIR; S12462; S12462.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;
KW   Transmembrane.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     60       POTENTIAL.
FT   DOMAIN       61    575       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    511    511       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   575 AA;  63347 MW;  93FD0532F6147BF6 CRC64;


  Query Match            100.0%;  Score 26;  DB 1;  Length 575;
  Best Local Similarity  100.0%;  Pred. No. 70;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     419 DRVYI 423


Search completed: July  1, 2002, 07:47:09
Job time: 475 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:13 ; Search time 122.73 Seconds
(without alignments)
7.048 Million cell updates/sec

Title: US-09-723-197-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 26 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 2 | 26 | 100.0 | 72 | 2 | Q9R540 | Q9r540 clostridium |
| 3 | 26 | 100.0 | 87 | 8 | Q9G9H0 | Q9g9h0 eretmocerus |
| 4 | 26 | 100.0 | 167 | 16 | Q9KG21 | Q9kg21 bacillus ha |
| 5 | 26 | 100.0 | 173 | 12 | Q88184 | Q88184 san miguel |
| 6 | 26 | 100.0 | 178 | 17 | Q9HIS3 | Q9his3 thermoplasm |
| 7 | 26 | 100.0 | 186 | 5 | Q9W387 | Q9w387 drosophila |
| 8 | 26 | 100.0 | 195 | 17 | O28741 | O28741 archaeoglob |
| 9 | 26 | 100.0 | 199 | 17 | Q973E6 | Q973e6 sulfolobus |
| 10 | 26 | 100.0 | 238 | 16 | O66729 | O66729 aquifex aeo |
| 11 | 26 | 100.0 | 245 | 6 | Q95J13 | Q95j13 pan troglod |
| 12 | 26 | 100.0 | 248 | 2 | Q44326 | Q44326 agrobacteri |
| 13 | 26 | 100.0 | 291 | 3 | Q9C445 | Q9c445 penicillium |
| 14 | 26 | 100.0 | 291 | 4 | Q9HBV1 | Q9hbv1 homo sapien |
| 15 | 26 | 100.0 | 291 | 11 | Q9ES81 | Q9es81 mus musculu |
| 16 | 26 | 100.0 | 295 | 4 | Q9HA44 | Q9ha44 homo sapien |
| 17 | 26 | 100.0 | 300 | 10 | Q94JW3 | Q94jw3 arabidopsis |
| 18 | 26 | 100.0 | 312 | 10 | O48726 | O48726 arabidopsis |
| 19 | 26 | 100.0 | 321 | 5 | Q9GNL3 | Q9gnl3 drosophila |
| 20 | 26 | 100.0 | 340 | 12 | Q9DVW3 | Q9dvw3 plutella xy |
| 21 | 26 | 100.0 | 369 | 13 | Q9IAE7 | Q9iae7 pantodon bu |
| 22 | 26 | 100.0 | 377 | 13 | Q9IAG5 | Q9iag5 gymnarchus |
| 23 | 26 | 100.0 | 408 | 10 | Q9MA64 | Q9ma64 arabidopsis |
| 24 | 26 | 100.0 | 409 | 17 | O27084 | O27084 methanother |
| 25 | 26 | 100.0 | 419 | 17 | Q973T1 | Q973t1 sulfolobus |
| 26 | 26 | 100.0 | 448 | 10 | Q94F16 | Q94f16 arabidopsis |
| 27 | 26 | 100.0 | 461 | 11 | Q9D2V0 | Q9d2v0 mus musculu |
| 28 | 26 | 100.0 | 477 | 4 | Q96FD5 | Q96fd5 homo sapien |
| 29 | 26 | 100.0 | 485 | 4 | Q96F91 | Q96f91 homo sapien |
| 30 | 26 | 100.0 | 485 | 6 | Q9GLP7 | Q9glp7 pan troglod |
| 31 | 26 | 100.0 | 485 | 6 | Q9GLP6 | Q9glp6 gorilla gor |
| 32 | 26 | 100.0 | 485 | 6 | Q9GLN8 | Q9gln8 pan troglod |
| 33 | 26 | 100.0 | 486 | 6 | Q9TSZ0 | Q9tsz0 callithrix |
| 34 | 26 | 100.0 | 486 | 13 | Q90XI3 | Q90xi3 chiloscylli |
| 35 | 26 | 100.0 | 509 | 10 | Q9T0L4 | Q9t014 arabidopsis |
| 36 | 26 | 100.0 | 509 | 10 | Q94AR8 | Q94ar8 arabidopsis |
| 37 | 26 | 100.0 | 575 | 12 | Q88413 | Q88413 sendai viru |
| 38 | 26 | 100.0 | 584 | 16 | Q97H15 | Q97h15 clostridium |
| 39 | 26 | 100.0 | 614 | 2 | O87250 | O87250 lactococcus |
| 40 | 26 | 100.0 | 644 | 16 | Q9KQX5 | Q9kqx5 vibrio chol |
| 41 | 26 | 100.0 | 661 | 16 | Q9KCM3 | Q9kcm3 bacillus ha |
| 42 | 26 | 100.0 | 749 | 16 | P73687 | P73687 synechocyst |
| 43 | 26 | 100.0 | 798 | 2 | Q9EZL3 | Q9ezl3 mycobacteri |
| 44 | 26 | 100.0 | 800 | 2 | Q93C65 | Q93c65 thermus aqu |
| 45 | 26 | 100.0 | 838 | 3 | O94653 | O94653 schizosacch |

ALIGNMENTS

RESULT 1
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

```
          |||||
Db      1 DRVYI 5


RESULT   2
Q9R540
ID   Q9R540      PRELIMINARY;      PRT;    72 AA.
AC   Q9R540;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   NEUROTOXIN HEAVY CHAIN 18 KDA FRAGMENT (FRAGMENT).
OS   Clostridium botulinum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1491;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94000342; PubMed=8397793;
RA   Gimenez J.A., DasGupta B.R.;
RT   "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72,
RT   45, 42, and 18 kD fragments.";
RL   J. Protein Chem. 12:351-363(1993).
DR   HSSP; P10845; 3BTA.
SQ   SEQUENCE   72 AA;  8165 MW;  B7A959576A615E18 CRC64;


  Query Match             100.0%;  Score 26;  DB 2;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     31 DRVYI 35


RESULT   3
Q9G9H0
ID   Q9G9H0      PRELIMINARY;      PRT;    87 AA.
AC   Q9G9H0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CYTOCHROME OXIDASE II (FRAGMENT).
OS   Eretmocerus mundus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Chalcidoidea; Aphelinidae; Eretmocerus.
OX   NCBI_TaxID=77302;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   De Barro P.J., Driver F., Naumann I.D., Clarke G.M., Curran J.;
RT   "Descriptions of three species of Eretmocerus Haldeman (Hymenoptera:
RT   Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
RT   Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
RT   Aleyrodidae) in Australia based on morphological and molecular data.";
RL   Aust. J. Entomol. 0:0-0(2000).
DR   EMBL; AF275275; AAG25079.1; -.
DR   InterPro; IPR001505; COX2.
DR   InterPro; IPR002429; Cyt_c_ox_2.
DR   Pfam; PF00116; COX2; 1.
DR   PRINTS; PR01166; CYCOXIDASEII.
DR   ProDom; PD000131; COX2; 1.
KW   Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER      87     87
SQ   SEQUENCE   87 AA;  10387 MW;  43E205FB2E1C6FEC CRC64;


  Query Match             100.0%;  Score 26;  DB 8;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     81 DRVYI 85


RESULT   4
Q9KG21
ID   Q9KG21      PRELIMINARY;      PRT;   167 AA.
AC   Q9KG21;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   BH0294 PROTEIN.
GN   BH0294.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
DR   EMBL; AP001508; BAB04013.1; -.
KW   Complete proteome.
SQ   SEQUENCE   167 AA;  19535 MW;  0C33F04D1A2E834D CRC64;


  Query Match             100.0%;  Score 26;  DB 16;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     61 DRVYI 65


RESULT   5
Q88184
ID   Q88184      PRELIMINARY;      PRT;   173 AA.
AC   Q88184;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   RNA-DEPENDENT RNA POLYMERASE (FRAGMENT).
OS   San Miguel sea lion virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC   Vesivirus.
OX   NCBI_TaxID=11982;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 5;
RX   MEDLINE=95287505; PubMed=7769708;
RA   Neill J.D., Meyer R.F., Seal B.S.;
RT   "Genetic relatedness of the caliciviruses: San Miguel sea lion and
RT   vesicular exanthema of swine viruses constitute a single genotype
RT   within the Caliciviridae.";
RL   J. Virol. 69:4484-4488(1995).
DR   EMBL; U18731; AAA82219.1; -.
DR   InterPro; IPR004004; Calici_pol_hel.
DR   PRINTS; PR00918; CALICVIRUSNS.
KW   RNA-directed RNA polymerase.
FT   NON_TER       1      1
FT   NON_TER     173    173
SQ   SEQUENCE   173 AA;  19532 MW;  1830C8461CC21F7F CRC64;
```

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  Query Match             100.0%;  Score 26;  DB 12;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     50 DRVYI 54


RESULT   6
Q9HIS3
ID   Q9HIS3      PRELIMINARY;      PRT;   178 AA.
AC   Q9HIS3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PROBABLE 50S RIBOSOMAL PROTEIN L6.
GN   TA1255.
OS   Thermoplasma acidophilum.
OC   Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
OC   Thermoplasma.
OX   NCBI_TaxID=2303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1728;
RX   MEDLINE=20479972; PubMed=11029001;
RA   Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA   Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT   "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT   acidophilum.";
RL   Nature 407:508-513(2000).
DR   EMBL; AL445067; CAC12379.1; -.
DR   InterPro; IPR000702; Ribosomal_L6.
DR   Pfam; PF00347; Ribosomal_L6; 1.
DR   ProDom; PD002236; Ribosomal_L6; 1.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE   178 AA;  19641 MW;  33B1312C268886A5 CRC64;


  Query Match             100.0%;  Score 26;  DB 17;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    134 DRVYI 138


RESULT   7
Q9W387
ID   Q9W387      PRELIMINARY;      PRT;   186 AA.
AC   Q9W387;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CG12664 PROTEIN.
GN   LD14 OR CG12664.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003446; AAF46447.1; -.
DR   FlyBase; FBgn0030090; ld14.
SQ   SEQUENCE   186 AA;  20461 MW;  D2B4ED097ACA6420 CRC64;


  Query Match             100.0%;  Score 26;  DB 5;  Length 186;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    110 DRVYI 114


RESULT   8
O28741
ID   O28741      PRELIMINARY;      PRT;   195 AA.
AC   O28741;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   CONSERVED HYPOTHETICAL PROTEIN.
GN   AF1531.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC   Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
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RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
DR   EMBL; AE000997; AAB89717.1; -.
DR   TIGR; AF1531; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   195 AA;  23194 MW;  C244F95420565E2C CRC64;
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  Query Match            100.0%;  Score 26;  DB 17;  Length 195;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     68 DRVYI 72
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RESULT   9
Q973E6
ID   Q973E6      PRELIMINARY;      PRT;   199 AA.
AC   Q973E6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN ST0953.
GN   ST0953.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000984; BAB65967.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   199 AA;  23401 MW;  7A42E708B18869D4 CRC64;
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  Query Match            100.0%;  Score 26;  DB 17;  Length 199;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
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Qy      1 DRVYI 5
          |||||
Db    144 DRVYI 148
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RESULT  10
O66729
ID   O66729      PRELIMINARY;      PRT;   238 AA.
AC   O66729;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ABC TRANSPORTER.
GN   ABCT7 OR AQ_413.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC       (ABC TRANSPORTERS).
DR   EMBL; AE000689; AAC06695.1; -.
DR   HSSP; Q58663; 1G6H.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Complete proteome; Transport.
SQ   SEQUENCE   238 AA;  26457 MW;  032A46CD90CEA8E5 CRC64;
```

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Qy      1 DRVYI 5
          |||||
Db    202 DRVYI 206
```

```
RESULT  11
Q95J13
ID   Q95J13      PRELIMINARY;      PRT;   245 AA.
AC   Q95J13;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
GN   REN.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=504, AND 505;
RA   Satta Y.;
RT   "Comparison of DNA and protein polymorphims between humans and
RT   chimpanzees.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062027; BAB55856.1; -.
DR   EMBL; AB062028; BAB55857.1; -.
FT   NON_TER     245    245
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Qy      1 DRVYI 5
          |||||
Db     34 DRVYI 38
```

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RESULT  12
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ID   Q44326      PRELIMINARY;      PRT;   248 AA.
AC   Q44326;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MOCC.
GN   MOCC.
```

```
OS   Agrobacterium tumefaciens.
OG   Plasmid Ti.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96236046; PubMed=8655509;
RA   Kim K.S., Farrand S.K.;
RT   "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT   opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT   region genes responsible for synthesis of this opine by the plant
RT   tumor.";
RL   J. Bacteriol. 178:3275-3284(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA   Farrand S.K.;
RT   "Octopine-type Ti plasmid sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC       (SDR) FAMILY.
DR   EMBL; AF242881; AAB07783.1; -.
DR   HSSP; O70351; 1E3S.
DR   InterPro; IPR002198; ADH_short.
DR   Pfam; PF00106; adh_short; 1.
DR   PRINTS; PR00080; SDRFAMILY.
KW   Oxidoreductase; Plasmid.
SQ   SEQUENCE   248 AA;  26810 MW;  10B69239CDEBB68D CRC64;


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Qy      1 DRVYI 5
          |||||
Db    221 DRVYI 225


RESULT  13
Q9C445
ID   Q9C445      PRELIMINARY;      PRT;   291 AA.
AC   Q9C445;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PAXU.
GN   PAXU.
OS   Penicillium paxilli.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=70109;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21106005; PubMed=11169115;
RA   Young C., McMillan L., Telfer E., Scott B.;
RT   "Molecular cloning and genetic analysis of an indole-diterpene gene
RT   cluster from Penicillium paxilli.";
RL   Mol. Microbiol. 39:754-764(2001).
DR   EMBL; AF279808; AAK11532.1; -.
SQ   SEQUENCE   291 AA;  32954 MW;  CFC35136FD40763E CRC64;


  Query Match             100.0%;  Score 26;  DB 3;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     16 DRVYI 20


RESULT  14
Q9HBV1
ID   Q9HBV1      PRELIMINARY;      PRT;   291 AA.
AC   Q9HBV1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   POPEYE PROTEIN 3.
GN   POP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20341060; PubMed=10882522;
RA   Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA   Jockusch H., Arnold H.H., Brand T.;
RT   "Isolation and characterization of the novel popeye gene family
RT   expressed in skeletal muscle and heart.";
RL   Dev. Biol. 223:371-382(2000).
DR   EMBL; AF204171; AAG23404.1; -.
SQ   SEQUENCE   291 AA;  33810 MW;  49B6EF5DBC02DDC2 CRC64;


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  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    248 DRVYI 252


RESULT  15
Q9ES81
ID   Q9ES81      PRELIMINARY;      PRT;   291 AA.
AC   Q9ES81;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   POPEYE PROTEIN 3.
GN   POP3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20341060; PubMed=10882522;
RA   Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA   Jockusch H., Arnold H.H., Brand T.;
RT   "Isolation and characterization of the novel popeye gene family
RT   expressed in skeletal muscle and heart.";
RL   Dev. Biol. 223:371-382(2000).
DR   EMBL; AF204176; AAG23409.1; -.
DR   MGD; MGI:1930153; Pop3.
SQ   SEQUENCE   291 AA;  33612 MW;  8AC6BFE107AEEE12 CRC64;


  Query Match             100.0%;  Score 26;  DB 11;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    248 DRVYI 252


Search completed: July  1, 2002, 07:45:14
Job time: 410 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds
(without alignments)
2.807 Million cell updates/sec

Title: US-09-723-197-10
Perfect score: 22
Sequence: 1 DRVY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 22 | 100.0 | 4 | 17 | AAR95671 | Angiotensin II fra |
| 2 | 22 | 100.0 | 4 | 19 | AAW64737 | Angiotensin II pep |
| 3 | 22 | 100.0 | 4 | 19 | AAW65606 | Angiotensin II ana |
| 4 | 22 | 100.0 | 4 | 19 | AAW71119 | Peptide AII(1-4) u |
| 5 | 22 | 100.0 | 4 | 20 | AAY49595 | Angiotensin analog |
| 6 | 22 | 100.0 | 4 | 20 | AAY33910 | Angiotensin II ana |
| 7 | 22 | 100.0 | 4 | 20 | AAY30548 | Amino acid sequenc |
| 8 | 22 | 100.0 | 4 | 20 | AAY30592 | Amino acid sequenc |
| 9 | 22 | 100.0 | 4 | 20 | AAY32723 | Angiotensin II ana |
| 10 | 22 | 100.0 | 4 | 20 | AAY33777 | Angiotensin II (AI |
| 11 | 22 | 100.0 | 4 | 20 | AAY15354 | Angiotensin II (AI |
| 12 | 22 | 100.0 | 4 | 20 | AAY15314 | Angiotensin II (AI |
| 13 | 22 | 100.0 | 4 | 21 | AAB27410 | Angiotensin II ana |
| 14 | 22 | 100.0 | 4 | 21 | AAB28108 | Angiotensin II ana |
| 15 | 22 | 100.0 | 4 | 21 | AAY84133 | Peptide comprising |
| 16 | 22 | 100.0 | 4 | 21 | AAY77046 | Angiotensin II (AI |
| 17 | 22 | 100.0 | 4 | 21 | AAY57410 | Angiotensin peptid |
| 18 | 22 | 100.0 | 4 | 22 | AAE08880 | AII peptide (resid |
| 19 | 22 | 100.0 | 4 | 22 | AAE02997 | Human angiotensin |
| 20 | 22 | 100.0 | 4 | 22 | AAE03160 | Human angiotensin |
| 21 | 22 | 100.0 | 4 | 22 | AAB91467 | Angiotensin peptid |
| 22 | 22 | 100.0 | 5 | 17 | AAR95670 | Angiotensin II fra |
| 23 | 22 | 100.0 | 5 | 19 | AAW64736 | Angiotensin II pep |
| 24 | 22 | 100.0 | 5 | 19 | AAW65605 | Angiotensin II ana |
| 25 | 22 | 100.0 | 5 | 19 | AAW71118 | Peptide AII(1-5) u |
| 26 | 22 | 100.0 | 5 | 20 | AAY49594 | Angiotensin analog |
| 27 | 22 | 100.0 | 5 | 20 | AAY33909 | Angiotensin II ana |
| 28 | 22 | 100.0 | 5 | 20 | AAY30547 | Amino acid sequenc |
| 29 | 22 | 100.0 | 5 | 20 | AAY30591 | Amino acid sequenc |
| 30 | 22 | 100.0 | 5 | 20 | AAY32722 | Angiotensin II ana |
| 31 | 22 | 100.0 | 5 | 20 | AAY33776 | Angiotensin II (AI |
| 32 | 22 | 100.0 | 5 | 20 | AAY15353 | Angiotensin II (AI |
| 33 | 22 | 100.0 | 5 | 20 | AAY15313 | Angiotensin II (AI |
| 34 | 22 | 100.0 | 5 | 21 | AAB27409 | Angiotensin II ana |
| 35 | 22 | 100.0 | 5 | 21 | AAB28107 | Angiotensin II ana |
| 36 | 22 | 100.0 | 5 | 21 | AAY84568 | Amino acid sequenc |
| 37 | 22 | 100.0 | 5 | 21 | AAY84132 | Peptide comprising |
| 38 | 22 | 100.0 | 5 | 21 | AAY77045 | Angiotensin II (AI |
| 39 | 22 | 100.0 | 5 | 21 | AAY57409 | Angiotensin peptid |
| 40 | 22 | 100.0 | 5 | 22 | AAE08879 | AII peptide (resid |
| 41 | 22 | 100.0 | 5 | 22 | AAE02996 | Human angiotensin |
| 42 | 22 | 100.0 | 5 | 22 | AAE03159 | Human angiotensin |
| 43 | 22 | 100.0 | 5 | 22 | AAB60413 | C-terminally trunc |
| 44 | 22 | 100.0 | 6 | 17 | AAR95669 | Angiotensin II fra |
| 45 | 22 | 100.0 | 6 | 19 | AAW65604 | Angiotensin II ana |

ALIGNMENTS

RESULT 1
AAR95671
ID AAR95671 standard; peptide; 4 AA.
XX
AC AAR95671;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(1-4).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
|||| 
Db 1 drvy 4

RESULT 2
AAW64737
ID AAW64737 standard; peptide; 4 AA.
XX
AC AAW64737;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #9.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
|||| 
Db 1 drvy 4

RESULT 3
AAW65606
ID AAW65606 standard; peptide; 4 AA.
XX
AC AAW65606;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-4).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 drvy 4

RESULT 4
AAW71119
ID AAW71119 standard; peptide; 4 AA.
XX
AC AAW71119;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-4) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 drvy 4

RESULT 5
AAY49595
ID AAY49595 standard; peptide; 4 AA.
XX
AC AAY49595;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:10.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

```
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT   6
AAY33910
ID   AAY33910 standard; peptide; 4 AA.
XX
AC   AAY33910;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Angiotensin II analogue AII(1-4).
XX
KW   embryonic stem cell; ES; angiotensin; totipotent cell;
KW   gene therapy; replacement therapy; angiotensin II; AII;
KW   analogue.
XX
OS   Homo sapiens.
XX
PN   WO9942122-A1.
XX
PD   26-AUG-1999.
XX
PF   16-FEB-1999;   99WO-US03243.
XX
PR   19-FEB-1998;   98US-0075179.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Dizerega G,  Rodgers KE;
XX
DR   WPI; 1999-527419/44.
XX
PT   Promoting embryonal cell proliferation, using angiotensinogen and
PT   angiotensin peptides, analogs or fragments
XX
PS   Claim 2; Page 8; 76pp; English.
XX
CC   This is the amino acid sequence of the Angiotensin II analogue,
CC   AII(1-4). The formation of Angiotensin II (AII) is initiated by the
CC   action of renin on the plasma substrate angiotensinogen.
CC   This results in Angiotensin I (AI) which then converted to AII by the
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY42372).
CC   Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC   analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC   or AII AT2 type 2 receptor agonists can rapidly provide a large
CC   population of ESCs (Embryonic Stem Cell) for use in replacement therapy.
CC   Similarly, methods that increase in vivo proliferation of ESCs will
CC   enhance the utility of replacement therapy by rapidly increasing local
CC   concentration of the stem cells and their progeny at the site of
CC   therapy. The method also increases the potential utility of ESCs as
CC   vehicles for gene therapy in certain disorders by more efficiently
CC   providing a large number of such cells for transfection, and also by
CC   providing a more efficient means to rapidly expand transfected ESCs.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 22;  DB 20;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT   7
```

```
AAY30548
ID   AAY30548 standard; peptide; 4 AA.
XX
AC   AAY30548;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII1-4.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents  -
XX
PS   Claim 2; Page 57; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 22;  DB 20;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT   8
AAY30592
ID   AAY30592 standard; peptide; 4 AA.
XX
AC   AAY30592;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII1-4.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
KW   gene therapy; hematopoietic disorder.
```

XX
OS Synthetic.
XX
PN WO9945945-A1.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05194.
XX
PR 10-MAR-1998; 98US-0077382.
PR 09-APR-1998; 98US-0081262.
PR 30-APR-1998; 98US-0083670.
PR 19-JUN-1998; 98US-0090096.
PR 22-JUN-1998; 98US-0090216.
PR 11-SEP-1998; 98US-0099957.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA (RODG/) RODGERS K E.
PA (DIZE/) DIZEREGA G.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551209/46.
XX
PT Use of angiotensin and angiotensin type peptides, for mitigating
PT radiation induced tissue damage, improving bone marrow transplantation
PT and promoting megakaryocyte and platelet production -
XX
PS Claim 2; Page 90; 116pp; English.
XX
CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes a method for mitigating
CC radiation induced tissue damage, improving the effectiveness of
CC radiation therapy, to support bone marrow transplantation, and
CC promoting megakaryocyte production and mobilization and platelet
CC production. The method comprises administration of the present peptides.
CC The methods can be used to mitigate radiation induced tissue damage, to
CC improve the effectiveness of radiation therapy, to support bone marrow
CC transplantation, and to promote megakaryocyte production and
CC mobilization and platelet production. They are used particularly in
CC cancer therapy. They can also be used to provide megakaryocytes as
CC vehicles for gene therapy in hematopoietic disorders, by providing a
CC more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
|||| 
Db 1 drvy 4

RESULT 9
AAY32723
ID AAY32723 standard; peptide; 4 AA.
XX
AC AAY32723;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-4).
XX
KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
|||| 
Db 1 drvy 4

RESULT 10
AAY33777
ID AAY33777 standard; peptide; 4 AA.
XX
AC AAY33777;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(1-4).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US03772.

XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 drvy 4

RESULT 11
AAY15354
ID AAY15354 standard; peptide; 4 AA.
XX
AC AAY15354;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-4).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX

PS Claim 2; Page 10; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 drvy 4

RESULT 12
AAY15314
ID AAY15314 standard; peptide; 4 AA.
XX
AC AAY15314;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-4).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a
CC decapeptide called angiotensin I (AI) which is converted to AII by the

```
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY15339).
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 22;  DB 20;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT  13
AAB27410
ID   AAB27410 standard; Peptide; 4 AA.
XX
AC   AAB27410;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Angiotensin II analog AII(1-4).
XX
KW   Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW   cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW   heart valve disease; myocarditis; angiotensin.
XX
OS   Synthetic.
XX
PN   WO200053211-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06198.
XX
PR   09-MAR-1999;   99US-0123678.
PR   31-AUG-1999;   99US-0151874.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-611400/58.
XX
PT   Promoting myocyte proliferation and myocardial tissue repair by
PT   contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT   for treating heart attacks, cardiomyopathies, inflammation and
PT   infection -
XX
PS   Claim 2; Page 10; 55pp; English.
XX
CC   The present invention relates to a method of promoting myocyte
CC   proliferation or differentiation by contacting myocytes with an active
CC   agent containing angiotensinogen, angiotensin I and II  (AI, AII), and
CC   angiotensin analogs. The present sequence is an angiotensin II analog
CC   of the invention. The active agents of the invention may be useful for
CC   promoting myocardial tissue repair following myocardial injury and for
CC   treating heart failure in a mammal. Administration to accelerate in
CC   vivo myocyte proliferation and/or to treat myocardial injuries can be
CC   used to treat cardiomyopathies, inflammation, infection, sepsis,
CC   ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC   ischemia and infarction and for improving cardiac output by increasing
CC   stroke volume.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 22;  DB 21;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT  14
AAB28108
ID   AAB28108 standard; Peptide; 4 AA.
XX
AC   AAB28108;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Angiotensin II analogue SEQ ID NO: 10.
XX
KW   Wound; scar formation; healing; adhesion formation; AII;
KW   angiotensin II analogue; scar treatment.
XX
OS   Synthetic.
XX
PN   WO200056345-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07669.
XX
PR   23-MAR-1999;   99US-0125707.
PR   16-JUN-1999;   99US-0139541.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-587607/55.
XX
PT   Limiting scar or adhesion formation comprises administering at least
PT   one active agent comprising a peptide -
XX
PS   Claim 2; Page 10; 54pp; English.
XX
CC   The present invention is concerned with peptide analogues of angiotensin
CC   II (AII) which can be used to limit scar and adhesion formation. The
CC   application of AII to wound tissue results in a rapid increase in the
CC   rate of wound healing and causes the proliferation of certain cells, such
CC   as epithelial cells and keratinocytes. Analogues of the protein have been
CC   shown to reduce scar formation, and can be used not only to limit new
CC   scar formation but also to therapeutically treat existing scars. The
CC   wound types include lacerations, burns, punctures, trauma, ulcers,
CC   periodontal conditions, laparotomy and incisional wounds, revision of
CC   hypertrophic scars, genetic hypertrophic scars, keloid scars,
CC   contractures after burns and cosmetic surgical procedures.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 22;  DB 21;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 drvy 4


RESULT  15
AAY84133
ID   AAY84133 standard; peptide; 4 AA.
XX
AC   AAY84133;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Peptide comprising amino acids 1-4 of angiotensin II.
```

XX
KW Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;
KW analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;
KW congestive heart disease; ischemic myocardial infarction;
KW embryonic development; wound healing; chronic inflammatory disease.
XX
OS Synthetic.
XX
PN WO200009144-A1.
XX
PD 24-FEB-2000.
XX
PF 12-AUG-1999; 99WO-US18374.
XX
PR 13-AUG-1998; 98US-0096414.
PR 18-SEP-1998; 98US-0101024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers K, Dizerega G;
XX
DR WPI; 2000-237409/20.
XX
PT Increasing blood flow to ischemic tissue for minimizing cardiac
PT remodelling and development of congestive heart failure involves
PT administration of an active agent -
XX
PS Claim 2; Page 42; 56pp; English.
XX
CC The present sequence represents an angiotensin II fragment. The
CC specification also describes peptides derived from angiotensinogen,
CC angiotensin I, angiotensin II, angiotensin III, and their analogues.
CC The peptides are used for increasing blood flow to ischemic tissue.
CC The peptides are angiogenesis stimulators. The peptides are useful for
CC increasing blood flow to ischemic tissue by stimulating angiogenesis,
CC and minimizing cardiac remodelling and development of congestive heart
CC disease following a ischemic myocardial infarction. The stimulation of
CC angiogenesis is also useful for embryonic development, wound healing
CC and treating chronic inflammatory disease.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 22; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 drvy 4

Search completed: July 1, 2002, 07:41:55
Job time: 347 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:01 ; Search time 59.1 Seconds
(without alignments)
1.653 Million cell updates/sec

Title: US-09-723-197-10
Perfect score: 22
Sequence: 1 DRVY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 22 | 100.0 | 4 | 2 | US-08-465-775-10 | Sequence 10, Appl |
| 2 | 22 | 100.0 | 4 | 3 | US-09-208-337-10 | Sequence 10, Appl |
| 3 | 22 | 100.0 | 4 | 3 | US-08-990-664-11 | Sequence 11, Appl |
| 4 | 22 | 100.0 | 4 | 4 | US-09-373-962-10 | Sequence 10, Appl |
| 5 | 22 | 100.0 | 4 | 4 | US-09-245-680-10 | Sequence 10, Appl |
| 6 | 22 | 100.0 | 4 | 4 | US-09-198-806C-10 | Sequence 10, Appl |
| 7 | 22 | 100.0 | 4 | 4 | US-09-352-191-10 | Sequence 10, Appl |
| 8 | 22 | 100.0 | 4 | 4 | US-09-012-400-10 | Sequence 10, Appl |
| 9 | 22 | 100.0 | 5 | 2 | US-08-465-775-9 | Sequence 9, Appli |
| 10 | 22 | 100.0 | 5 | 3 | US-09-208-337-9 | Sequence 9, Appli |
| 11 | 22 | 100.0 | 5 | 3 | US-08-990-664-10 | Sequence 10, Appl |
| 12 | 22 | 100.0 | 5 | 4 | US-09-373-962-9 | Sequence 9, Appli |
| 13 | 22 | 100.0 | 5 | 4 | US-09-245-680-9 | Sequence 9, Appli |
| 14 | 22 | 100.0 | 5 | 4 | US-09-198-806C-9 | Sequence 9, Appli |
| 15 | 22 | 100.0 | 5 | 4 | US-09-352-191-9 | Sequence 9, Appli |
| 16 | 22 | 100.0 | 5 | 4 | US-09-012-400-9 | Sequence 9, Appli |
| 17 | 22 | 100.0 | 6 | 2 | US-08-465-775-8 | Sequence 8, Appli |
| 18 | 22 | 100.0 | 6 | 3 | US-09-208-337-8 | Sequence 8, Appli |
| 19 | 22 | 100.0 | 6 | 3 | US-08-990-664-9 | Sequence 9, Appli |
| 20 | 22 | 100.0 | 6 | 4 | US-09-373-962-8 | Sequence 8, Appli |
| 21 | 22 | 100.0 | 6 | 4 | US-09-245-680-8 | Sequence 8, Appli |
| 22 | 22 | 100.0 | 6 | 4 | US-09-198-806C-8 | Sequence 8, Appli |
| 23 | 22 | 100.0 | 6 | 4 | US-09-352-191-8 | Sequence 8, Appli |
| 24 | 22 | 100.0 | 6 | 4 | US-09-012-400-8 | Sequence 8, Appli |
| 25 | 22 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 26 | 22 | 100.0 | 7 | 2 | US-09-047-594-1 | Sequence 1, Appli |
| 27 | 22 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 28 | 22 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
| 29 | 22 | 100.0 | 7 | 4 | US-09-373-962-4 | Sequence 4, Appli |
| 30 | 22 | 100.0 | 7 | 4 | US-09-245-680-4 | Sequence 4, Appli |
| 31 | 22 | 100.0 | 7 | 4 | US-09-198-806C-4 | Sequence 4, Appli |
| 32 | 22 | 100.0 | 7 | 4 | US-09-352-191-4 | Sequence 4, Appli |
| 33 | 22 | 100.0 | 7 | 4 | US-09-012-400-4 | Sequence 4, Appli |
| 34 | 22 | 100.0 | 7 | 6 | 5451571-4 | Patent No. 5451571 |
| 35 | 22 | 100.0 | 8 | 1 | US-07-858-842-2 | Sequence 2, Appli |
| 36 | 22 | 100.0 | 8 | 1 | US-08-021-839A-3 | Sequence 3, Appli |
| 37 | 22 | 100.0 | 8 | 1 | US-08-184-935-2 | Sequence 2, Appli |
| 38 | 22 | 100.0 | 8 | 1 | US-08-212-433A-29 | Sequence 29, Appl |
| 39 | 22 | 100.0 | 8 | 1 | US-08-185-448-8 | Sequence 8, Appli |
| 40 | 22 | 100.0 | 8 | 1 | US-07-776-272-1 | Sequence 1, Appli |
| 41 | 22 | 100.0 | 8 | 1 | US-08-428-488-21 | Sequence 21, Appl |
| 42 | 22 | 100.0 | 8 | 1 | US-08-337-781-1 | Sequence 1, Appli |
| 43 | 22 | 100.0 | 8 | 1 | US-08-240-711-20 | Sequence 20, Appl |
| 44 | 22 | 100.0 | 8 | 1 | US-08-594-117-1 | Sequence 1, Appli |
| 45 | 22 | 100.0 | 8 | 1 | US-08-594-117-3 | Sequence 3, Appli |

ALIGNMENTS

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US-08-465-775-10
; Sequence 10, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-10


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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
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Db       1 DRVY 4
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US-09-208-337-10
; Sequence 10, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-10


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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
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Db      1 DRVY 4


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; Sequence 11, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-11


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Qy      1 DRVY 4
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Db      1 DRVY 4


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US-09-373-962-10
; Sequence 10, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   .TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-373-962-10


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  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
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Db      1 DRVY 4
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US-09-245-680-10
; Sequence 10, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-245-680-10


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Qy      1 DRVY 4
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Db      1 DRVY 4


RESULT   6
US-09-198-806C-10
; Sequence 10, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-198-806C-10


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   7
US-09-352-191-10
; Sequence 10, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-352-191-10


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
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Db      1 DRVY 4


RESULT   8
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; Sequence 10, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-012-400-10


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Qy      1 DRVY 4
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Db      1 DRVY 4


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; Sequence 9, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/465,775
;      FILING DATE:
;      CLASSIFICATION: 514
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Spitals, John P.
;      REGISTRATION NUMBER: 29,215
;      REFERENCE/DOCKET NUMBER: 1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (213) 977-1001
;      TELEFAX: (213) 977-1003
;  INFORMATION FOR SEQ ID NO: 9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 5 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;    MOLECULE TYPE: peptide
US-08-465-775-9


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 DRVY 4


RESULT 10
US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT: Rodgers, Kathleen
;    APPLICANT: Gere, diZerega
;    TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES: 15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Knobbe, Martens, Olson & Bear
;      STREET: 620 Newport Center Drive 16th Floor
;      CITY: Newport Beach
;      STATE: CA
;      COUNTRY: U.S.A.
;      ZIP: 92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/465,775
;      FILING DATE: 06-JUN-1995
;      APPLICATION NUMBER: 08/337,781
;      FILING DATE: 14-NOV-1994
;      APPLICATION NUMBER: 08/126,368
;      FILING DATE: 24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Altman, Daniel E
;      REGISTRATION NUMBER: 34,115
;      REFERENCE/DOCKET NUMBER: USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 949-760-0404
;      TELEFAX: 949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO: 9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 5 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: Peptide
US-09-208-337-9


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Db      1 DRVY 4


RESULT 11
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT: Rodgers, Kathleen
;    APPLICANT: diZerega, Gere
;    TITLE OF INVENTION: METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION: IN SKIN GRAFTS
;    NUMBER OF SEQUENCES: 46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Knobbe, Martens, Olson & Bear
;      STREET: 620 Newport Center Drive 16th Floor
;      CITY: Newport Beach
;      STATE: CA
;      COUNTRY: U.S.A.
;      ZIP: 92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 60/028,310
;      FILING DATE: 16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Altman, Daniel E
;      REGISTRATION NUMBER: 34,115
;      REFERENCE/DOCKET NUMBER: USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 714-760-0404
;      TELEFAX: 714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO: 10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 5 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: peptide
US-08-990-664-10


  Query Match           100.0%;  Score 22;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 DRVY 4


RESULT  12
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-373-962-9


  Query Match             100.0%;  Score 22;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT  13
US-09-245-680-9
; Sequence 9, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-245-680-9


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Qy      1 DRVY 4
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Db      1 DRVY 4


RESULT  14
US-09-198-806C-9
; Sequence 9, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-198-806C-9


  Query Match             100.0%;  Score 22;  DB 4;  Length 5;
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Qy      1 DRVY 4
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Db      1 DRVY 4


RESULT  15
US-09-352-191-9
; Sequence 9, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-352-191-9


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  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


Search completed: July  1, 2002, 07:43:01
Job time: 302 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:30 ; Search time 69.93 Seconds
(without alignments)
5.496 Million cell updates/sec

Title: US-09-723-197-10
Perfect score: 22
Sequence: 1 DRVY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 22 | 100.0 | 10 | 2 | A60624 | angiotensin I - Ja |
| 2 | 22 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 3 | 22 | 100.0 | 10 | 2 | A90917 | angiotensin precur |
| 4 | 22 | 100.0 | 10 | 2 | A90345 | angiotensin precur |
| 5 | 22 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 6 | 22 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 7 | 22 | 100.0 | 43 | 2 | S42852 | melA protein - Sal |
| 8 | 22 | 100.0 | 52 | 2 | T15646 | hypothetical prote |
| 9 | 22 | 100.0 | 54 | 2 | PT0194 | protein-tyrosine k |
| 10 | 22 | 100.0 | 54 | 2 | PT0189 | protein-tyrosine k |
| 11 | 22 | 100.0 | 74 | 2 | H70944 | hypothetical prote |
| 12 | 22 | 100.0 | 84 | 2 | A95174 | hypothetical prote |
| 13 | 22 | 100.0 | 84 | 2 | B99040 | hypothetical prote |
| 14 | 22 | 100.0 | 88 | 2 | E90169 | hypothetical prote |
| 15 | 22 | 100.0 | 92 | 2 | T18731 | hypothetical prote |
| 16 | 22 | 100.0 | 99 | 2 | C69025 | conserved hypothet |
| 17 | 22 | 100.0 | 101 | 2 | G81116 | hypothetical prote |
| 18 | 22 | 100.0 | 113 | 2 | PN0091 | alpha-dextrin endo |
| 19 | 22 | 100.0 | 113 | 2 | A96960 | hypothetical prote |
| 20 | 22 | 100.0 | 115 | 2 | A48793 | glycosylation-inhi |
| 21 | 22 | 100.0 | 115 | 2 | I52370 | macrophage migrati |
| 22 | 22 | 100.0 | 115 | 2 | A44499 | macrophage migrati |
| 23 | 22 | 100.0 | 115 | 2 | C47274 | migration inhibito |
| 24 | 22 | 100.0 | 121 | 2 | H87615 | conserved hypothet |
| 25 | 22 | 100.0 | 124 | 2 | B70472 | flagellar protein |
| 26 | 22 | 100.0 | 124 | 2 | E90326 | hypothetical prote |
| 27 | 22 | 100.0 | 126 | 2 | S31027 | gene 82 protein - |
| 28 | 22 | 100.0 | 128 | 2 | T30432 | hypothetical prote |
| 29 | 22 | 100.0 | 133 | 2 | AE2202 | hypothetical prote |
| 30 | 22 | 100.0 | 135 | 2 | G86695 | hypothetical prote |
| 31 | 22 | 100.0 | 137 | 1 | I40658 | methylaspartate mu |
| 32 | 22 | 100.0 | 137 | 1 | S29502 | methylaspartate mu |
| 33 | 22 | 100.0 | 137 | 2 | T41575 | ubiquinol-cytochro |
| 34 | 22 | 100.0 | 139 | 2 | E72856 | AcOrf-53 protein - |
| 35 | 22 | 100.0 | 142 | 2 | T12987 | hypothetical prote |
| 36 | 22 | 100.0 | 144 | 2 | E87693 | conserved hypothet |
| 37 | 22 | 100.0 | 144 | 2 | T22423 | hypothetical prote |
| 38 | 22 | 100.0 | 146 | 2 | T10325 | hypothetical prote |
| 39 | 22 | 100.0 | 147 | 2 | T35696 | xylanase A - Strep |
| 40 | 22 | 100.0 | 157 | 2 | G00016 | FGF-receptor - com |
| 41 | 22 | 100.0 | 158 | 2 | D90391 | conserved hypothet |
| 42 | 22 | 100.0 | 159 | 2 | F86400 | hypothetical prote |
| 43 | 22 | 100.0 | 160 | 2 | T15925 | hypothetical prote |
| 44 | 22 | 100.0 | 160 | 2 | AF2171 | hypothetical prote |
| 45 | 22 | 100.0 | 161 | 2 | AD0360 | conserved hypothet |

ALIGNMENTS

RESULT 1
A60624
angiotensin I - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of t
A;Reference number: A60624; MUID:90284684
A;Accession: A60624
A;Molecule type: protein
A;Residues: 1-10 <TAK>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
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Db 1 DRVY 4

RESULT 2
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
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Db 1 DRVY 4

RESULT 3
A90917
angiotensin precursor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90917; A01250
R;Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A;Reference number: A90917; MUID:74127845
A;Accession: A90917
A;Molecule type: protein
A;Residues: 1-10 <NAK>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 DRVY 4

RESULT 4
A90345
angiotensin precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90345; A01250
R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 DRVY 4

RESULT 5
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 22; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 DRVY 4

RESULT 6
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 22; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 1 DRVY 4

RESULT 7
S42852
melA protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 22-Jun-1999
C;Accession: S42852
R;Mizushima, K.; Awakihara, S.; Kuroda, M.; Ishikawa, T.; Tsuda, M.; Tsuchiya, T.
Mol. Gen. Genet. 234, 74-80, 1992
A;Title: Cloning and sequencing of the melB gene encoding the melibiose permease of S
A;Reference number: S23576; MUID:92357019
A;Accession: S42852
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-43 <MIZ>
A;Cross-references: EMBL:X62101; NID:g450672; PIDN:CAA44010.1; PID:g450673
C;Superfamily: melibiose-specific alpha-galactosidase

Query Match 100.0%; Score 22; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
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Db 1 DRVY 4

RESULT 8
T15646
hypothetical protein C26F1.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15646
R;Geisel, C.; Stellyes, L.; Bradshaw, H.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C26F1.

A;Reference number: Z18381
A;Accession: T15646
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-52 <GEI>
A;Cross-references: EMBL:U53148; NID:g1255375; PID:g1255385; PIDN:AAB37072.1; GSPDB:GN0
A;Experimental source: strain Bristol N2; clone C26F1
C;Genetics:
A;Gene: CESP:C26F1.10
A;Map position: 5
A;Introns: 29/1

Query Match 100.0%; Score 22; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
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Db 41 DRVY 44

RESULT 9
PT0194
protein-tyrosine kinase (EC 2.7.1.112) tyro-12 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 10-Sep-1997
C;Accession: PT0194
R;Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differentially expressed in
A;Reference number: PT0183; MUID:91222560
A;Accession: PT0194
A;Molecule type: mRNA
A;Residues: 1-54 <LAI>
A;Experimental source: sciatic nerve
C;Genetics:
A;Gene: tyro-12
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;1-54/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 47 DRVY 50

RESULT 10
PT0189
protein-tyrosine kinase (EC 2.7.1.112) tyro-7 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 04-Feb-2000
C;Accession: PT0189
R;Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differentially expressed in
A;Reference number: PT0183; MUID:91222560
A;Accession: PT0189
A;Molecule type: mRNA
A;Residues: 1-54 <LAI>
A;Experimental source: sciatic nerve
C;Genetics:
A;Gene: tyro-7
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;1-54/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 47 DRVY 50

RESULT 11
H70944
hypothetical protein Rv2049c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70944
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987
A;Accession: H70944
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-74 <COL>
A;Cross-references: GB:AL021899; GB:AL123456; NID:g3242282; PIDN:CAA17263.1; PID:e125
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2049c

Query Match 100.0%; Score 22; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 27 DRVY 30

RESULT 12
A95174
hypothetical protein SP1494 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: A95174
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75586.1; PID:g14972984; GSPDB:GN00164; TIGR:
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1494

Query Match 100.0%; Score 22; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 66 DRVY 69

RESULT 13
B99040
hypothetical protein spr1347 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: B99040
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B99040
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00151.1; PID:g15458994; GSPDB:GN00174
C;Genetics:
A;Gene: spr1347

Query Match 100.0%; Score 22; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 66 DRVY 69

RESULT 14
E90169
hypothetical protein SSO5544 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: E90169
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <KUR>
A;Cross-references: GB:AE006641; NID:g13813414; PIDN:AAK40612.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO5544

Query Match 100.0%; Score 22; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
||||
Db 84 DRVY 87

RESULT 15
T18731
hypothetical protein B0391.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18731
R;Gardner, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19012
A;Accession: T18731
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-92 <WIL>
A;Cross-references: EMBL:Z81454; PIDN:CAB03802.1; GSPDB:GN00023; CESP:B0391.10
A;Experimental source: clone B0391
C;Genetics:
A;Gene: CESP:B0391.10
A;Map position: 5
A;Introns: 18/1

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVY 4
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Db 56 DRVY 59

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:09 ; Search time 34.05 Seconds
(without alignments)
4.549 Million cell updates/sec

Title: US-09-723-197-10
Perfect score: 22
Sequence: 1 DRVY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 22 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 22 | 100.0 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 3 | 22 | 100.0 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 4 | 22 | 100.0 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 5 | 22 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 6 | 22 | 100.0 | 99 | 1 | YB87_METTH | O27255 methanobact |
| 7 | 22 | 100.0 | 114 | 1 | MIF_CHICK | Q02960 gallus gall |
| 8 | 22 | 100.0 | 114 | 1 | MIF_HUMAN | P14174 homo sapien |
| 9 | 22 | 100.0 | 114 | 1 | MIF_MOUSE | P34884 mus musculu |
| 10 | 22 | 100.0 | 114 | 1 | MIF_RAT | P30904 rattus norv |
| 11 | 22 | 100.0 | 126 | 1 | VG82_BPML5 | Q05298 mycobacteri |
| 12 | 22 | 100.0 | 137 | 1 | MAMA_CLOCO | P80078 clostridium |
| 13 | 22 | 100.0 | 137 | 1 | MAMA_CLOTT | Q05488 clostridium |
| 14 | 22 | 100.0 | 137 | 1 | UCR7_SCHPO | O74533 schizosacch |
| 15 | 22 | 100.0 | 139 | 1 | Y053_NPVAC | P41457 autographa |
| 16 | 22 | 100.0 | 146 | 1 | Y053_NPVOP | O10310 orgyia pseu |
| 17 | 22 | 100.0 | 161 | 1 | RNPA_HELPJ | Q9zjh0 helicobacte |
| 18 | 22 | 100.0 | 161 | 1 | RNPA_HELPY | P55997 helicobacte |
| 19 | 22 | 100.0 | 162 | 1 | MCRW_METTH | Q50485 methanobact |
| 20 | 22 | 100.0 | 174 | 1 | YA68_METTH | O27140 methanobact |
| 21 | 22 | 100.0 | 177 | 1 | Y552_TREPA | O83563 treponema p |
| 22 | 22 | 100.0 | 178 | 1 | NADM_METTH | O26253 methanobact |
| 23 | 22 | 100.0 | 181 | 1 | NIP7_YEAST | Q08962 saccharomyc |
| 24 | 22 | 100.0 | 183 | 1 | SOMA_PRIGL | P34006 prionace gl |
| 25 | 22 | 100.0 | 190 | 1 | SOMA_BALBO | P33092 balaenopter |
| 26 | 22 | 100.0 | 190 | 1 | SOMA_LAMPA | P37885 lama guanic |
| 27 | 22 | 100.0 | 190 | 1 | SOMA_LOXAF | P20392 loxodonta a |
| 28 | 22 | 100.0 | 190 | 1 | SOMA_VULVU | P10766 vulpes vulp |
| 29 | 22 | 100.0 | 191 | 1 | SOMA_CHEMY | P34005 chelonia my |
| 30 | 22 | 100.0 | 201 | 1 | ARA5_ARAHY | P04149 arachis hyp |
| 31 | 22 | 100.0 | 215 | 1 | SOMA_MONDO | Q9gl60 monodelphis |
| 32 | 22 | 100.0 | 215 | 1 | SOMA_RANCA | P10813 rana catesb |
| 33 | 22 | 100.0 | 215 | 1 | SOMA_TRIVU | O62754 trichosurus |
| 34 | 22 | 100.0 | 216 | 1 | SOMA_CANFA | P33711 canis famil |
| 35 | 22 | 100.0 | 216 | 1 | SOMA_FELCA | P46404 felis silve |
| 36 | 22 | 100.0 | 216 | 1 | SOMA_HORSE | P01245 equus cabal |
| 37 | 22 | 100.0 | 216 | 1 | SOMA_MESAU | P37886 mesocricetu |
| 38 | 22 | 100.0 | 216 | 1 | SOMA_MOUSE | P06880 mus musculu |
| 39 | 22 | 100.0 | 216 | 1 | SOMA_MUSVI | P19795 mustela vis |
| 40 | 22 | 100.0 | 216 | 1 | SOMA_PIG | P01248 sus scrofa |
| 41 | 22 | 100.0 | 216 | 1 | SOMA_RABIT | P46407 oryctolagus |
| 42 | 22 | 100.0 | 216 | 1 | SOMA_RAT | P01244 rattus norv |
| 43 | 22 | 100.0 | 217 | 1 | SOMA_BOVIN | P01246 bos taurus |
| 44 | 22 | 100.0 | 217 | 1 | SOMA_BUBBU | O18938 bubalus bub |
| 45 | 22 | 100.0 | 217 | 1 | SOMA_CEREL | P56437 cervus elap |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 22; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVY 4
          ||||
Db      1 DRVY 4
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RESULT 2
ANG1_BOTJA
ID ANG1_BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

```
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1308 MW;  CEF50DD761F2DB42 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   3
ANGT_BOVIN
ID   ANGT_BOVIN     STANDARD;      PRT;    10 AA.
AC   P01017;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RA   Elliott D.F., Peart W.S.;
RT   "The amino acid sequence in a hypertensin.";
RL   Biochem. J. 65:246-254(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90345; A90345.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1282 MW;  CEEFBDD761F2DB42 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   4
ANGT_CHICK
ID   ANGT_CHICK     STANDARD;      PRT;    10 AA.
AC   P01018;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken;
RX   MEDLINE=74127845; PubMed=4361802;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. 3. Structure of fowl
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 21:2085-2087(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=90284684; PubMed=2191893;
RA   Takei Y., Hasegawa Y.;
RT   "Vasopressor and depressor effects of native angiotensins and
RT   inhibition of these effects in the Japanese quail.";
RL   Gen. Comp. Endocrinol. 79:12-22(1990).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90917; A90917.
DR   PIR; A60624; A60624.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1232 MW;  CEFBEDD761F2DB42 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   5
ANGT_HORSE
ID   ANGT_HORSE     STANDARD;      PRT;    14 AA.
AC   P01016;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE.
RA   Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT   "The preparation, purification, and amino acid sequence of a
RT   polypeptide renin substrate.";
RL   J. Exp. Med. 106:439-453(1957).
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CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   6
YB87_METTH
ID   YB87_METTH     STANDARD;      PRT;    99 AA.
AC   O27255;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MTH1187.
GN   MTH1187.
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000887; AAB85676.1; -.
DR   InterPro; IPR002767; DUF77.
DR   Pfam; PF01910; DUF77; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   99 AA;  10798 MW;  32D48B66A74C7430 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     70 DRVY 73


RESULT   7
MIF_CHICK
ID   MIF_CHICK      STANDARD;      PRT;   114 AA.
AC   Q02960;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase).
GN   MIF.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M95776; AAA48939.1; -.
DR   PIR; C47274; C47274.
DR   HSSP; P34884; 1MFI.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine.
FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
FT   INIT_MET      0      0       BY SIMILARITY.
SQ   SEQUENCE   114 AA;  12353 MW;  A55222D00E6D05CF CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     92 DRVY 95


RESULT   8
MIF_HUMAN
ID   MIF_HUMAN      STANDARD;      PRT;   114 AA.
AC   P14174;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
```

```
DE   tautomerase) (Glycosylation-inhibiting factor) (GIF).
GN   MIF OR MMIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90017510; PubMed=2552447;
RA   Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,
RA   Clark S.C., David J.R.;
RT   "Molecular cloning of a cDNA encoding a human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245178; PubMed=8188240;
RA   Paralkar V., Wistow G.J.;
RT   "Cloning the human gene for macrophage migration inhibitory factor
RT   (MIF).";
RL   Genomics 19:48-51(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,
RA   Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE OF 9-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [5]
RP   SEQUENCE OF 1-10.
RC   TISSUE=Liver;
RX   MEDLINE=93162045; PubMed=1286669;
RA   Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA   Appel R.D., Hughes G.J.;
RT   "Human liver protein map: a reference database established by
RT   microsequencing and gel comparison.";
RL   Electrophoresis 13:992-1001(1992).
RN   [6]
RP   SEQUENCE OF 2-23.
RX   MEDLINE=93256574; PubMed=7683862;
RA   Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gabius H.J.;
RT   "The major binding protein of the interferon antagonist sarcolectin
RT   in human placenta is a macrophage migration inhibitory factor.";
RL   Arch. Biochem. Biophys. 303:74-80(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=96338096; PubMed=8766818;
RA   Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;
RT   "Crystal structure of macrophage migration inhibitory factor from
RT   human lymphocyte at 2.1-A resolution.";
RL   FEBS Lett. 389:145-148(1996).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=96181524; PubMed=8610159;
RA   Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Mikayama T.,
RA   Ishizaka K., Kuroki R.;
RT   "The crystal structure of human glycosylation-inhibiting factor is a
RT   trimeric barrel with three 6-stranded beta-sheets.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=96224258; PubMed=8643551;
RA   Sun H.W., Bernhagen J., Bucala R., Lolis E.;
RT   "Crystal structure at 2.6-A resolution of human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=99282199; PubMed=10353846;
RA   Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;
RT   "Pro-1 of macrophage migration inhibitory factor functions as a
RT   catalytic base in the phenylpyruvate tautomerase activity.";
RL   Biochemistry 38:7346-7354(1999).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE
CC       SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA
CC       OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF
CC       CHRONIC INFLAMMATORY LOCI.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; Z23063; CAA80598.1; -.
DR   EMBL; M25639; AAA36315.1; -.
DR   EMBL; M95775; AAA36179.1; -.
DR   EMBL; L10612; AAA35892.1; -.
DR   EMBL; L19686; AAA21814.1; -.
DR   PIR; A33838; A33838.
DR   PIR; S33277; S33277.
DR   PDB; 1GIF; 12-MAR-97.
DR   PDB; 1MIF; 07-DEC-96.
DR   PDB; 1P1G; 07-JUN-99.
DR   PDB; 1CGQ; 07-JUN-99.
DR   PDB; 1CA7; 30-JUN-99.
DR   SWISS-2DPAGE; P14174; HUMAN.
DR   Siena-2DPAGE; P14174; -.
DR   MIM; 153620; -.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
FT   CONFLICT    105    105       N -> S (IN REF. 1).
SQ   SEQUENCE   114 AA;  12345 MW;  4BD525232B3F3069 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db      92 DRVY 95


RESULT   9
MIF_MOUSE
ID   MIF_MOUSE      STANDARD;      PRT;   114 AA.
AC   P34884;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Delayed early response protein 6) (DER6) (Glycosylation-
DE   inhibiting factor).
GN   MIF.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC   TISSUE=Pituitary;
RX   MEDLINE=94019845; PubMed=8413654;
RA   Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,
RA   Tracey K.J., Voelter W., Manogue K.R., Cerami A., Bucala R.;
RT   "MIF is a pituitary-derived cytokine that potentiates lethal
RT   endotoxaemia.";
RL   Nature 365:756-759(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=92375060; PubMed=1508193;
RA   Lanahan A., Williams J.B., Sanders L.K., Nathans D.;
RT   "Growth factor-induced delayed early response genes.";
RL   Mol. Cell. Biol. 12:3919-3929(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,
RA   Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=95221891; PubMed=7706726;
RA   Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,
RA   Bucala R.;
RT   "Cloning and characterization of the gene for mouse macrophage
RT   migration inhibitory factor (MIF).";
RL   J. Immunol. 154:3863-3870(1995).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047325; PubMed=7558021;
RA   Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,
RA   Copeland N.G., David J.R., Gerard C.;
RT   "Structural characterization and chromosomal location of the mouse
RT   macrophage migration inhibitory factor gene and pseudogenes.";
RL   Genomics 27:412-419(1995).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047324; PubMed=7558020;
RA   Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,
RA   Wistow G.;
RT   "Genomic cloning of mouse MIF (macrophage inhibitory factor) and
RT   genetic mapping of the human and mouse expressed gene and nine mouse
RT   pseudogenes.";
RL   Genomics 27:405-411(1995).
RN   [7]
RP   SEQUENCE OF 5-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX   MEDLINE=99303983; PubMed=10360941;
RA   Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L.,
RA   Whitman C.P.;
RT   "Crystal structure of macrophage migration inhibitory factor
RT   complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution:
RT   implications for enzymatic catalysis and inhibition.";
RL   Biochemistry 38:7444-7452(1999).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).
RX   MEDLINE=20393856; PubMed=10933783;
RA   Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;
RT   "Mechanism of the phenylpyruvate tautomerase activity of macrophage
RT   migration inhibitory factor: properties of the P1G, P1A, Y95F, and
RT   N97A mutants.";
RL   Biochemistry 39:9671-9678(2000).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23048; CAA80583.1; -.
DR   EMBL; U19825; AAA91637.1; -.
DR   EMBL; L10613; AAA37693.1; -.
DR   EMBL; U20156; AAA91638.1; -.
DR   EMBL; L39357; AAA74321.1; -.
DR   EMBL; L07607; AAA37111.1; -.
DR   PIR; S34299; S34299.
DR   PIR; A44499; A44499.
DR   PDB; 1MFF; 11-AUG-00.
DR   PDB; 1MFI; 22-JUN-99.
DR   MGD; MGI:96982; Mif.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
SQ   SEQUENCE   114 AA;  12373 MW;  8FD2339CF0792F9E CRC64;


  Query Match            100.0%;  Score 22;  DB 1;  Length 114;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db      92 DRVY 95


RESULT  10
MIF_RAT
ID   MIF_RAT        STANDARD;      PRT;   114 AA.
AC   P30904;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Glutathione-binding 13 kDa protein).
GN   MIF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95038523; PubMed=7951062;
RA   Sakai M., Nishihira J., Hibiya Y., Koyama Y., Nishi S.;
RT   "Glutathione binding rat liver 13k protein is the homologue of the
RT   macrophage migration inhibitory factor.";
RL   Biochem. Mol. Biol. Int. 33:439-446(1994).
```

```
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RA   Wen Y., Li G., Bekhor I.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PVG/C;
RA   Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B.,
RA   Reynolds A.J., Whitehouse C.J.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-25.
RX   MEDLINE=93063370; PubMed=1436109;
RA   Blocki F.A., Schlievert P.M., Wackett L.P.;
RT   "Rat liver protein linking chemical and immunological detoxification
RT   systems.";
RL   Nature 360:269-270(1992).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC   TISSUE=Liver;
RX   MEDLINE=96186248; PubMed=8605628;
RA   Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J.,
RA   Sakai M.;
RT   "Crystal structure of the macrophage migration inhibitory factor from
RT   rat liver.";
RL   Nat. Struct. Biol. 3:259-266(1996).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS
CC       INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S73424; AAB32392.1; -.
DR   EMBL; U20999; AAA62644.1; -.
DR   EMBL; U62326; AAB04024.1; -.
DR   PDB; 1FIM; 11-JUL-96.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
FT   CONFLICT     50     50       S -> R (IN REF. 2).
SQ   SEQUENCE   114 AA;  12346 MW;  9E33C39CF064329E CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     92 DRVY 95


RESULT  11
VG82_BPML5
ID   VG82_BPML5     STANDARD;      PRT;   126 AA.
AC   Q05298;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Gene 82 protein (GP82).
GN   82.
OS   Mycobacteriophage L5.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=31757;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93211282; PubMed=8459766;
RA   Hatfull G.F., Sarkis G.J.;
RT   "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT   a phage system for mycobacterial genetics.";
RL   Mol. Microbiol. 7:395-405(1993).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z18946; CAA79458.1; -.
DR   PIR; S31027; S31027.
SQ   SEQUENCE   126 AA;  14167 MW;  7D1188C3B2CAC8C6 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db    114 DRVY 117


RESULT  12
MAMA_CLOCO
ID   MAMA_CLOCO     STANDARD;      PRT;   137 AA.
AC   P80078; Q60144;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Methylaspartate mutase S chain (EC 5.4.99.1) (Glutamate mutase sigma
DE   subunit).
GN   MAMA OR GLMS.
OS   Clostridium cochlearium.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1494;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1285 / ATCC 17787;
RX   MEDLINE=95094816; PubMed=7880251;
RA   Zelder O., Beatrix B., Leutbecher U., Buckel W.;
RT   "Characterization of the coenzyme-B12-dependent glutamate mutase from
RT   Clostridium cochlearium produced in Escherichia coli.";
RL   Eur. J. Biochem. 226:577-585(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1285 / ATCC 17787;
RX   MEDLINE=94283856; PubMed=8013871;
RA   Zelder O., Beatrix B., Buckel W.;
RT   "Cloning, sequencing and expression in Escherichia coli of the gene
RT   encoding component S of the coenzyme B12-dependent glutamate mutase
RT   from Clostridium cochlearium.";
RL   FEMS Microbiol. Lett. 118:15-21(1994).
RN   [3]
RP   SEQUENCE OF 1-23.
RC   STRAIN=DSM 1285 / ATCC 17787;
RX   MEDLINE=92241315; PubMed=1315276;
RA   Leutbecher U., Boecher R., Linder D., Buckel W.;
RT   "Glutamate mutase from Clostridium cochlearium. Purification,
RT   cobamide content and stereospecific inhibitors.";
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RL   Eur. J. Biochem. 205:759-765(1992).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC   STRAIN=DSM 1285 / ATCC 17787;
RX   MEDLINE=99404935; PubMed=10467146;
RA   Reitzer R., Gruber K., Jogl G., Wagner U.G., Bothe H., Buckel W.,
RA   Kratky C.;
RT   "Glutamate mutase from Clostridium cochlearium: the structure of a
RT   coenzyme B12-dependent enzyme provides new mechanistic insights.";
RL   Structure 7:891-902(1999).
CC   -!- CATALYTIC ACTIVITY: L-threo-3-methylaspartate = L-glutamate.
CC   -!- COFACTOR: 5'-deoxy-5'-adenosyl-adeninylcobamide (pseudo-coenzyme
CC       B12).
CC   -!- PATHWAY: Fermentation of glutamate; first step.
CC   -!- SUBUNIT: Heterotetramer of 2 E subunits and 2 S subunits.
CC   -!- SIMILARITY: CONTAINS 1 B12-BINDING DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80997; CAA56921.1; -.
DR   EMBL; X75890; CAA53484.1; -.
DR   PIR; S21249; S21249.
DR   PDB; 1CB7; 28-FEB-00.
DR   PDB; 1CCW; 01-MAR-00.
DR   InterPro; IPR003312; B12-binding.
DR   Pfam; PF02310; B12-binding; 1.
KW   Isomerase; Cobalt; Vitamin B12; 3D-structure.
FT   METAL        16     16       COBALT.
SQ   SEQUENCE   137 AA;  14812 MW;  D9C5BF8DE5D1E878 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db     114 DRVY 117


RESULT  13
MAMA_CLOTT
ID   MAMA_CLOTT     STANDARD;      PRT;   137 AA.
AC   Q05488;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Methylaspartate mutase S chain (EC 5.4.99.1) (Glutamate mutase sigma
DE   subunit).
GN   MAMA OR MUTS.
OS   Clostridium tetanomorphum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1553;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-33.
RC   STRAIN=NCIMB 11547;
RX   MEDLINE=93011908; PubMed=1397267;
RA   Marsh E.N.G., Holloway D.E.;
RT   "Cloning and sequencing of glutamate mutase component S from
RT   Clostridium tetanomorphum. Homologies with other cobalamin-dependent
RT   enzymes.";
RL   FEBS Lett. 310:167-170(1992).
RN   [2]
RP   SEQUENCE OF 1-24.
RC   STRAIN=H1 / DSM 528;
RX   MEDLINE=93202282; PubMed=8454064;
RA   Brecht M., Kellermann J., Plueckthun A.;
RT   "Cloning and sequencing of glutamate mutase component E from
RT   Clostridium tetanomorphum.";
RL   FEBS Lett. 319:84-89(1993).
RN   [3]
RP   STRUCTURE BY NMR.
RC   STRAIN=ATCC 15920;
RX   MEDLINE=98416697; PubMed=9739092;
RA   Tollinger M., Konrat R., Hilbert B.H., Marsh E.N.G., Kraeutler B.;
RT   "How a protein prepares for B12 binding: structure and dynamics of
RT   the B12-binding subunit of glutamate mutase from Clostridium
RT   tetanomorphum.";
RL   Structure 6:1021-1033(1998).
CC   -!- CATALYTIC ACTIVITY: L-threo-3-methylaspartate = L-glutamate.
CC   -!- COFACTOR: 5'-deoxy-5'-adenosyl-adeninylcobamide (pseudo-coenzyme
CC       B12).
CC   -!- PATHWAY: Fermentation of glutamate; first step.
CC   -!- SUBUNIT: Heterotetramer of 2 E subunits and 2 S subunits. E exists
CC       as a homodimer and S as a monomer.
CC   -!- SIMILARITY: CONTAINS 1 B12-BINDING DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X70499; CAA49908.1; -.
DR   EMBL; X68570; CAA48567.1; -.
DR   PIR; S29502; S29502.
DR   PDB; 1BE1; 26-AUG-98.
DR   InterPro; IPR003312; B12-binding.
DR   Pfam; PF02310; B12-binding; 1.
KW   Isomerase; Cobalt; Vitamin B12; 3D-structure.
SQ   SEQUENCE   137 AA;  14748 MW;  E71FE55BA8CE3DB3 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db     114 DRVY 117


RESULT  14
UCR7_SCHPO
ID   UCR7_SCHPO     STANDARD;      PRT;   137 AA.
AC   O74533;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable ubiquinol-cytochrome C reductase complex 14 kDa protein
DE   (EC 1.10.2.2) (Complex III subunit VII).
GN   SPCC737.02C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Murphy L., Harris D., Lyne M.H., Rajandream M.A., Barrell B.G.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
CC       REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH
CC       IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THIS COMPONENT
CC       IS INVOLVED IN REDOX-LINKED PROTON PUMPING (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
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```
CC       ferrocytochrome c.
CC   -!- SUBUNIT: FUNGI BC1 COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY
CC       SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (Potential).
CC   -!- SIMILARITY: BELONGS TO THE UQCRB/QCR7 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   ---------------------------------------------------------------------
DR   EMBL; AL031546; CAA20859.1; -.
DR   InterPro; IPR003197; UCR_14kD.
DR   Pfam; PF02271; UCR_14kD; 1.
KW   Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
KW   Oxidoreductase.
SQ   SEQUENCE   137 AA;  16030 MW;  36CEF418C9E02994 CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db      65 DRVY 68


RESULT  15
Y053_NPVAC
ID   Y053_NPVAC     STANDARD;      PRT;   139 AA.
AC   P41457;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Hypothetical 17.0 kDa protein in LEF8-FP intergenic region.
OS   Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC   Nucleopolyhedrovirus.
OX   NCBI_TaxID=46015;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C6;
RX   MEDLINE=94303173; PubMed=8030224;
RA   Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT   "The complete DNA sequence of Autographa californica nuclear
RT   polyhedrosis virus.";
RL   Virology 202:586-605(1994).
CC   -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L22858; AAA66683.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   139 AA;  16995 MW;  C03632331F01EA3A CRC64;


  Query Match             100.0%;  Score 22;  DB 1;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db     109 DRVY 112


Search completed: July  1, 2002, 07:47:10
Job time: 476 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:14 ; Search time 122.73 Seconds
(without alignments)
5.638 Million cell updates/sec

Title: US-09-723-197-10
Perfect score: 22
Sequence: 1 DRVY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 22 | 100.0 | 10 | 13 | Q9PS07 | Q9ps07 alligator m |
| 2 | 22 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 3 | 22 | 100.0 | 52 | 5 | Q18234 | Q18234 caenorhabdi |
| 4 | 22 | 100.0 | 53 | 12 | Q86959 | Q86959 human papil |
| 5 | 22 | 100.0 | 54 | 4 | Q9UD27 | Q9ud27 homo sapien |
| 6 | 22 | 100.0 | 55 | 5 | Q9TX23 | Q9tx23 hirudo medi |
| 7 | 22 | 100.0 | 56 | 13 | Q91995 | Q91995 xenopus lae |
| 8 | 22 | 100.0 | 57 | 13 | Q08556 | Q08556 phasianidae |
| 9 | 22 | 100.0 | 57 | 13 | Q08555 | Q08555 phasianidae |
| 10 | 22 | 100.0 | 61 | 10 | Q9LJT0 | Q9ljt0 arabidopsis |
| 11 | 22 | 100.0 | 64 | 4 | Q9NPE3 | Q9npe3 homo sapien |
| 12 | 22 | 100.0 | 64 | 5 | Q9V5P6 | Q9v5p6 drosophila |
| 13 | 22 | 100.0 | 64 | 11 | Q9CQS2 | Q9cqs2 mus musculu |
| 14 | 22 | 100.0 | 66 | 5 | O76159 | O76159 dugesia jap |
| 15 | 22 | 100.0 | 67 | 13 | Q90957 | Q90957 gallus gall |
| 16 | 22 | 100.0 | 68 | 13 | Q9YI21 | Q9yi21 gallus gall |
| 17 | 22 | 100.0 | 72 | 2 | Q9R540 | Q9r540 clostridium |
| 18 | 22 | 100.0 | 74 | 16 | O53491 | O53491 mycobacteri |
| 19 | 22 | 100.0 | 78 | 11 | O55059 | O55059 rattus norv |
| 20 | 22 | 100.0 | 82 | 12 | Q91LD0 | Q91ld0 white spot |
| 21 | 22 | 100.0 | 84 | 16 | Q97PU8 | Q97pu8 streptococc |
| 22 | 22 | 100.0 | 87 | 8 | Q9G9H0 | Q9g9h0 eretmocerus |
| 23 | 22 | 100.0 | 88 | 10 | Q93YK7 | Q93yk7 brassica na |
| 24 | 22 | 100.0 | 88 | 17 | Q980L8 | Q98018 sulfolobus |
| 25 | 22 | 100.0 | 89 | 10 | Q94H51 | Q94h51 oryza sativ |
| 26 | 22 | 100.0 | 91 | 10 | Q9FIY3 | Q9fiy3 arabidopsis |
| 27 | 22 | 100.0 | 91 | 17 | Q975V9 | Q975v9 sulfolobus |
| 28 | 22 | 100.0 | 92 | 5 | O62015 | O62015 caenorhabdi |
| 29 | 22 | 100.0 | 95 | 5 | Q9NM38 | Q9nm38 leishmania |
| 30 | 22 | 100.0 | 99 | 15 | Q907E4 | Q907e4 human immun |
| 31 | 22 | 100.0 | 101 | 16 | Q9JS54 | Q9js54 neisseria m |
| 32 | 22 | 100.0 | 104 | 15 | Q99CQ9 | Q99cq9 human immun |
| 33 | 22 | 100.0 | 104 | 15 | Q99CN4 | Q99cn4 human immun |
| 34 | 22 | 100.0 | 107 | 15 | O57063 | O57063 chimpanzee |
| 35 | 22 | 100.0 | 109 | 4 | Q9H500 | Q9h500 homo sapien |
| 36 | 22 | 100.0 | 110 | 6 | Q9N265 | Q9n265 bos taurus |
| 37 | 22 | 100.0 | 113 | 16 | Q97LR6 | Q97lr6 clostridium |
| 38 | 22 | 100.0 | 115 | 12 | Q91I61 | Q91i61 regina rana |
| 39 | 22 | 100.0 | 119 | 2 | Q9L5D3 | Q9l5d3 comamonas t |
| 40 | 22 | 100.0 | 120 | 6 | Q9TSG0 | Q9tsg0 ovis aries |
| 41 | 22 | 100.0 | 120 | 16 | Q98EF4 | Q98ef4 rhizobium l |
| 42 | 22 | 100.0 | 121 | 11 | Q9CVB5 | Q9cvb5 mus musculu |
| 43 | 22 | 100.0 | 121 | 16 | Q9A481 | Q9a481 caulobacter |
| 44 | 22 | 100.0 | 122 | 2 | Q46219 | Q46219 clostridium |
| 45 | 22 | 100.0 | 124 | 16 | O67806 | O67806 aquifex aeo |

ALIGNMENTS

RESULT 1
Q9PS07
ID Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANGIOTENSIN I, ANG I.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RX MEDLINE=93307610; PubMed=8319878;
RA Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA Stephens G.A., Sakakibara S.;
RT "New angiotensin I isolated from a reptile, Alligator
RT mississippiensis.";
RL Gen. Comp. Endocrinol. 90:214-219(1993).
SQ SEQUENCE 10 AA; 1216 MW; CEE38DD761F2DB42 CRC64;

Query Match 100.0%; Score 22; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVY 4
          ||||
Db      1 DRVY 4
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RESULT 2
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

```
DE   ANGIOTENSINOGEN (FRAGMENT).
OS   Theromyzon tessulatum (Leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX   NCBI_TaxID=13286;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95365039; PubMed=7637887;
RA   Laurent V., Bulet P., Salzet M.A.;
RT   "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT   molecule with forms of vertebrate angiotensinogens: a hormonal system
RT   conserved in the course of evolution.";
RL   Neurosci. Lett. 190:175-178(1995).
RN   [2]
RP   SEQUENCE OF 1-10.
RC   TISSUE=BRAIN;
RX   MEDLINE=96201949; PubMed=8612806;
RA   Laurent V., Salzet M.;
RT   "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT   tessulatum.";
RL   FEBS Lett. 384:123-127(1996).
CC   -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW   Glycoprotein; Serpin.
FT   NON_TER      14      14
SQ   SEQUENCE   14 AA;  1763 MW;  335109D8EEEFBDD7 CRC64;

  Query Match             100.0%;  Score 22;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db      1 DRVY 4


RESULT   3
Q18234
ID   Q18234      PRELIMINARY;      PRT;    52 AA.
AC   Q18234;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   C26F1.10 PROTEIN.
GN   C26F1.10.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Geisel C., Stellyes L., Bradshaw H.;
RT   "The sequence of C. elegans cosmid C26F1.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U53148; AAB37072.1; -.
SQ   SEQUENCE   52 AA;  5932 MW;  5D05D734A309F1F2 CRC64;

  Query Match             100.0%;  Score 22;  DB 5;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     41 DRVY 44


RESULT   4
Q86959
ID   Q86959      PRELIMINARY;      PRT;    53 AA.
AC   Q86959;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   E1 (E1) (FRAGMENT).
GN   E1.
OS   Human papillomavirus type 2.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=35256;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L1;
RX   MEDLINE=96037380; PubMed=7473271;
RA   Padayachee A., Sanders C.M., Maitland N.J.;
RT   "A polymerase chain reaction (PCR) investigation of oral verrucae
RT   which contain HPV types 2 and 57 by in situ hybridization.";
RL   J. Oral Pathol. Med. 24:329-334(1995).
DR   EMBL; S80058; AAB35445.2; -.
FT   NON_TER       1       1
FT   NON_TER      53      53
SQ   SEQUENCE   53 AA;  5628 MW;  8F6CCF2A510C209E CRC64;

  Query Match             100.0%;  Score 22;  DB 12;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     40 DRVY 43


RESULT   5
Q9UD27
ID   Q9UD27      PRELIMINARY;      PRT;    54 AA.
AC   Q9UD27;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AXL RECEPTOR TYROSINE KINASE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95204052; PubMed=7896447;
RA   Craven R.J., Xu L.H., Weiner T.M., Fridell Y.W., Dent G.A.,
RA   Srivastava S., Varnum B., Liu E.T., Cance W.G.;
RT   "Receptor tyrosine kinases expressed in metastatic colon cancer.";
RL   Int. J. Cancer 60:791-797(1995).
DR   InterPro; IPR000719; Euk_pkinase.
```

```
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   54 AA;  6164 MW;  FE3D169C1CD954C1 CRC64;


  Query Match             100.0%;  Score 22;  DB 4;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     47 DRVY 50


RESULT   6
Q9TX23
ID   Q9TX23      PRELIMINARY;      PRT;    55 AA.
AC   Q9TX23;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LPTK55=PDGF RECEPTOR TYROSINE KINASE HOMOLOG.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95330783; PubMed=7606763;
RA   Nitabach M.N., Macagno E.R.;
RT   "Cell- and tissue-specific expression of putative protein kinase mRNAs
RT   in the embryonic leech, Hirudo medicinalis.";
RL   Cell Tissue Res. 280:479-489(1995).
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   55 AA;  6369 MW;  AFED1C7D06C5785B CRC64;


  Query Match             100.0%;  Score 22;  DB 5;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     48 DRVY 51


RESULT   7
Q91995
ID   Q91995      PRELIMINARY;      PRT;    56 AA.
AC   Q91995;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PROTEIN-TYROSINE KINASE (G62) (FRAGMENT).
GN   G62 OR E7.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYO;
RX   MEDLINE=95383727; PubMed=7655077;
RA   Brandli A.W., Kirschner M.W.;
RT   "Molecular cloning of tyrosine kinases in the early Xenopus embryo:
RT   identification of Eck-related genes expressed in cranial neural crest
RT   cells of the second (hyoid) arch.";
RL   Dev. Dyn. 203:119-140(1995).
DR   EMBL; U11730; AAA91293.1; -.
DR   EMBL; U11720; AAA91283.1; -.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase; Tyrosine-protein kinase.
FT   NON_TER       1      1
FT   NON_TER      56     56
SQ   SEQUENCE   56 AA;  6408 MW;  BD31D90C5791B45F CRC64;


  Query Match             100.0%;  Score 22;  DB 13;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     49 DRVY 52


RESULT   8
Q08556
ID   Q08556      PRELIMINARY;      PRT;    57 AA.
AC   Q08556;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   QUAIL DNA FOR FIBROBLAST GROWTH FACTOR RECEPTOR (CLONE H7)
DE   (FRAGMENT).
OS   Phasianidae.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes.
OX   NCBI_TaxID=9005;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93096482; PubMed=1281306;
RA   Marcelle C., Eichmann A.;
RT   "Molecular cloning of a family of protein kinase genes expressed in
RT   the avian embryo.";
RL   Oncogene 7:2479-2487(1992).
DR   EMBL; X69693; CAA49363.1; -.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR000719;. Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Receptor; Transferase.
FT   NON_TER       1      1
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6523 MW;  8DAA6A71E3F1B45E CRC64;


  Query Match             100.0%;  Score 22;  DB 13;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     50 DRVY 53


RESULT   9
Q08555
ID   Q08555      PRELIMINARY;      PRT;    57 AA.
AC   Q08555;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   QUAIL DNA FOR TYROSINE KINASE RECEPTOR (PDGFR/FMS) (CLONE CK1)
DE   (FRAGMENT).
OS   Phasianidae.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes.
```

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OX   NCBI_TaxID=9005;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93096482; PubMed=1281306;
RA   Marcelle C., Eichmann A.;
RT   "Molecular cloning of a family of protein kinase genes expressed in
RT   the avian embryo.";
RL   Oncogene 7:2479-2487(1992).
DR   EMBL; X69694; CAA49364.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Receptor; Transferase.
FT   NON_TER       1      1
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6586 MW;  AB0689E2ED7B58ED CRC64;


  Query Match             100.0%;  Score 22;  DB 13;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     50 DRVY 53


RESULT  10
Q9LJT0
ID   Q9LJT0      PRELIMINARY;      PRT;    61 AA.
AC   Q9LJT0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SIMILARITY TO LYSYL-TRNA SYNTHETASE.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20363099; PubMed=10907853;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT   Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT   TAC and BAC clones.";
RL   DNA Res. 7:217-221(2000).
DR   EMBL; AP000411; BAB02142.1; -.
DR   HSSP; P14825; 1LYL.
DR   InterPro; IPR004364; tRNA-synt_2.
DR   InterPro; IPR002313; tRNA-synt_lys_2.
DR   Pfam; PF00152; tRNA-synt_2; 1.
DR   PRINTS; PR00982; TRNASYNTHLYS.
KW   Aminoacyl-tRNA synthetase.
SQ   SEQUENCE   61 AA;  7075 MW;  A8E725C053AFB2C4 CRC64;


  Query Match             100.0%;  Score 22;  DB 10;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     44 DRVY 47


RESULT  11
Q9NPE3
ID   Q9NPE3      PRELIMINARY;      PRT;    64 AA.
AC   Q9NPE3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NOP10P (NUCLEOLAR PROTEIN FAMILY A, MEMBER 3) (H/ACA SMALL NUCLEOLAR
DE   RNPS).
GN   NOP10.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Toji S., Yano M., Tamai K.;
RT   "Human Nop10p cDNA.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99059744; PubMed=9843512;
RA   Henras A., Henry Y., Bousquet-Antonelli C., Noaillac-Depeyre J.,
RA   Gelugne J., Caizergues-Ferrer M.;
RT   "Nhp2p and Nop10p are essential for the function of H/ACA snoRNPs.";
RL   EMBO J. 17:7078-7090(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Toji S., Yano M., Tamai K.;
RT   "Human Nop10p genomic DNA.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB043104; BAA96133.1; -.
DR   EMBL; AB043103; BAA96107.1; -.
DR   EMBL; BC008886; AAH08886.1; -.
SQ   SEQUENCE   64 AA;  7706 MW;  62E9BCFFB27036FA CRC64;


  Query Match             100.0%;  Score 22;  DB 4;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     12 DRVY 15


RESULT  12
Q9V5P6
ID   Q9V5P6      PRELIMINARY;      PRT;    64 AA.
AC   Q9V5P6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CG7637 PROTEIN.
GN   CG7637.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003828; AAF58753.1; -.
DR   FlyBase; FBgn0033548; CG7637.
SQ   SEQUENCE   64 AA;  7634 MW;  B957575E84DEA7CF CRC64;


  Query Match             100.0%;  Score 22;  DB 5;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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Qy      1 DRVY 4
          ||||
Db     12 DRVY 15


RESULT  13
Q9CQS2
ID   Q9CQS2      PRELIMINARY;      PRT;    64 AA.
AC   Q9CQS2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1110036B12RIK PROTEIN.
GN   1110036B12RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012875; BAB28529.1; -.
DR   EMBL; AK004120; BAB23180.1; -.
DR   MGD; MGI:1913431; 1110036B12Rik.
SQ   SEQUENCE   64 AA;  7706 MW;  62E9BCFFB27036FA CRC64;


  Query Match             100.0%;  Score 22;  DB 11;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     12 DRVY 15


RESULT  14
O76159
ID   O76159      PRELIMINARY;      PRT;    66 AA.
AC   O76159;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RECEPTOR TYROSINE KINASE (FRAGMENT).
OS   Dugesia japonica (Planarian).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Paludicola; Dugesiidae; Dugesia.
OX   NCBI_TaxID=6161;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GI;
RX   MEDLINE=98340876; PubMed=9675112;
RA   Ogawa K., Wakayama A., Kunisada T., Orii H., Watanabe K., Agata K.;
RT   "Identification of a receptor tyrosine kinase involved in germ cell
RT   differentiation in planarians.";
RL   Biochem. Biophys. Res. Commun. 248:204-209(1998).
DR   EMBL; AB014498; BAA32049.1; -.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Transferase.
FT   NON_TER       1      1
FT   NON_TER      66     66
SQ   SEQUENCE   66 AA;  7709 MW;  09D367D0E95F04B2 CRC64;


  Query Match             100.0%;  Score 22;  DB 5;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVY 4
          ||||
Db     53 DRVY 56


RESULT  15
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ID   Q90957      PRELIMINARY;      PRT;    67 AA.
AC   Q90957;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PROTEIN-TYROSINE KINASE (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LENS;
RA   Potts J.D., Harocopos G.J., Beebe D.C.;
RT   "Identification of receptor tyrosine kinases in the embryonic chicken
RT   lens.";
RL   Curr. Eye Res. 0:0-0(1993).
DR   EMBL; L20623; AAA49043.1; -.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Transferase.
FT   NON_TER       1      1
FT   NON_TER      67     67
SQ   SEQUENCE   67 AA;  7856 MW;  F6EFB106477A9AB1 CRC64;


  Query Match             100.0%;  Score 22;  DB 13;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVY 4
           ||||
Db      55 DRVY 58


Search completed: July  1, 2002, 07:45:16
Job time: 412 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:41:55 ; Search time 158.26 Seconds
(without alignments)
2.106 Million cell updates/sec

Title: US-09-723-197-11
Perfect score: 15
Sequence: 1 DRV 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 15 | 100.0 | 3 | 19 | AAW64738 | Angiotensin II pep |
| 2 | 15 | 100.0 | 3 | 19 | AAW71120 | Peptide AII(1-3) u |
| 3 | 15 | 100.0 | 3 | 20 | AAY30549 | Amino acid sequenc |
| 4 | 15 | 100.0 | 3 | 20 | AAY30593 | Amino acid sequenc |
| 5 | 15 | 100.0 | 3 | 21 | AAY84134 | Peptide comprising |
| 6 | 15 | 100.0 | 4 | 17 | AAR95671 | Angiotensin II fra |
| 7 | 15 | 100.0 | 4 | 19 | AAW64737 | Angiotensin II pep |
| 8 | 15 | 100.0 | 4 | 19 | AAW65606 | Angiotensin II ana |
| 9 | 15 | 100.0 | 4 | 19 | AAW71119 | Peptide AII(1-4) u |
| 10 | 15 | 100.0 | 4 | 19 | AAW61302 | Peptide 17 used to |
| 11 | 15 | 100.0 | 4 | 19 | AAW61138 | Peptide 17 used to |
| 12 | 15 | 100.0 | 4 | 19 | AAW47218 | Variant MHC Class |
| 13 | 15 | 100.0 | 4 | 20 | AAY49595 | Angiotensin analog |
| 14 | 15 | 100.0 | 4 | 20 | AAY33910 | Angiotensin II ana |
| 15 | 15 | 100.0 | 4 | 20 | AAY30548 | Amino acid sequenc |
| 16 | 15 | 100.0 | 4 | 20 | AAY30592 | Amino acid sequenc |
| 17 | 15 | 100.0 | 4 | 20 | AAY32723 | Angiotensin II ana |
| 18 | 15 | 100.0 | 4 | 20 | AAY33777 | Angiotensin II (AI |
| 19 | 15 | 100.0 | 4 | 20 | AAY15354 | Angiotensin II (AI |
| 20 | 15 | 100.0 | 4 | 20 | AAY15314 | Angiotensin II (AI |
| 21 | 15 | 100.0 | 4 | 21 | AAB27410 | Angiotensin II ana |
| 22 | 15 | 100.0 | 4 | 21 | AAB28108 | Angiotensin II ana |
| 23 | 15 | 100.0 | 4 | 21 | AAY84133 | Peptide comprising |
| 24 | 15 | 100.0 | 4 | 21 | AAY77046 | Angiotensin II (AI |
| 25 | 15 | 100.0 | 4 | 21 | AAY57410 | Angiotensin peptid |
| 26 | 15 | 100.0 | 4 | 22 | AAE08880 | AII peptide (resid |
| 27 | 15 | 100.0 | 4 | 22 | AAE02997 | Human angiotensin |
| 28 | 15 | 100.0 | 4 | 22 | AAE03160 | Human angiotensin |
| 29 | 15 | 100.0 | 4 | 22 | AAB91467 | Angiotensin peptid |
| 30 | 15 | 100.0 | 5 | 8 | AAP71638 | Diuretic peptide d |
| 31 | 15 | 100.0 | 5 | 11 | AAR09372 | Sequence of atrial |
| 32 | 15 | 100.0 | 5 | 14 | AAR65519 | Endothelin antagon |
| 33 | 15 | 100.0 | 5 | 17 | AAR95670 | Angiotensin II fra |
| 34 | 15 | 100.0 | 5 | 18 | AAW31079 | Mugwort pollen all |
| 35 | 15 | 100.0 | 5 | 19 | AAW64736 | Angiotensin II pep |
| 36 | 15 | 100.0 | 5 | 19 | AAW65605 | Angiotensin II ana |
| 37 | 15 | 100.0 | 5 | 19 | AAW71118 | Peptide AII(1-5) u |
| 38 | 15 | 100.0 | 5 | 19 | AAW75554 | M. tuberculosis 80 |
| 39 | 15 | 100.0 | 5 | 19 | AAW37888 | Mycobacterium tube |
| 40 | 15 | 100.0 | 5 | 20 | AAY49594 | Angiotensin analog |
| 41 | 15 | 100.0 | 5 | 20 | AAY33909 | Angiotensin II ana |
| 42 | 15 | 100.0 | 5 | 20 | AAY30547 | Amino acid sequenc |
| 43 | 15 | 100.0 | 5 | 20 | AAY30591 | Amino acid sequenc |
| 44 | 15 | 100.0 | 5 | 20 | AAY32722 | Angiotensin II ana |
| 45 | 15 | 100.0 | 5 | 20 | AAY33776 | Angiotensin II (AI |

ALIGNMENTS

RESULT 1
AAW64738
ID AAW64738 standard; peptide; 3 AA.
XX
AC AAW64738;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #10.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;

XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 3 AA;

Query Match 100.0%; Score 15; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 drv 3

RESULT 2
AAW71120
ID AAW71120 standard; peptide; 3 AA.
XX
AC AAW71120;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-3) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 3 AA;

Query Match 100.0%; Score 15; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 drv 3

RESULT 3
AAY30549
ID AAY30549 standard; peptide; 3 AA.
XX
AC AAY30549;
XX
DT 18-NOV-1999 (first entry)
XX
DE Amino acid sequence of angiotensin II fragment AII1-3.
XX
KW Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS Synthetic.
XX
PN WO9946285-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05261.
XX
PR 11-MAR-1998; 98US-0077499.
PR 12-JUN-1998; 98US-0089064.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551360/46.
XX
PT An improved method for producing a tissue equivalent with angiotensin I
PT and II derived active agents -
XX
PS Claim 2; Page 10; 83pp; English.
XX
CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes an improved method
CC for producing a tissue equivalent. The method comprises contacting
CC the tissue equivalent with angiotensin I and II derived active
CC agents. The methods are used for production and culture of tissue
CC equivalents (three-dimensional cell and tissue culture systems),
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC vascular graft, cartilage, ligament, collagen lattice, liver and
CC kidney tissue equivalents. The methods and tissue culture systems
CC are used for the long-term proliferation of cells and tissues
CC in an in vitro environment that more closely approximates that found

```
CC   in vivo.
XX
SQ   Sequence   3 AA;


  Query Match           100.0%;  Score 15;  DB 20;  Length 3;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 drv 3


RESULT   4
AAY30593
ID   AAY30593 standard; peptide; 3 AA.
XX
AC   AAY30593;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII1-3.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
KW   gene therapy; hematopoietic disorder.
XX
OS   Synthetic.
XX
PN   WO9945945-A1.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05194.
XX
PR   10-MAR-1998;   98US-0077382.
PR   09-APR-1998;   98US-0081262.
PR   30-APR-1998;   98US-0083670.
PR   19-JUN-1998;   98US-0090096.
PR   22-JUN-1998;   98US-0090216.
PR   11-SEP-1998;   98US-0099957.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA   (RODG/) RODGERS K E.
PA   (DIZE/) DIZEREGA G.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551209/46.
XX
PT   Use of angiotensin and angiotensin type peptides, for mitigating
PT   radiation induced tissue damage, improving bone marrow transplantation
PT   and promoting megakaryocyte and platelet production  -
XX
PS   Claim 2; Page 90; 116pp; English.
XX
CC   AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes a method for mitigating
CC   radiation induced tissue damage, improving the effectiveness of
CC   radiation therapy, to support bone marrow transplantation, and
CC   promoting megakaryocyte production and mobilization and platelet
CC   production. The method comprises administration of the present peptides.
CC   The methods can be used to mitigate radiation induced tissue damage, to
CC   improve the effectiveness of radiation therapy, to support bone marrow
CC   transplantation, and to promote megakaryocyte production and
CC   mobilization and platelet production. They are used particularly in
CC   cancer therapy. They can also be used to provide megakaryocytes as
CC   vehicles for gene therapy in hematopoietic disorders, by providing a
CC   more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ   Sequence   3 AA;


  Query Match           100.0%;  Score 15;  DB 20;  Length 3;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 drv 3


RESULT   5
AAY84134
ID   AAY84134 standard; peptide; 3 AA.
XX
AC   AAY84134;
XX
DT   03-JUL-2000  (first entry)
XX
DE   Peptide comprising amino acids 1-3 of angiotensin II.
XX
KW   Angiotensin III; angiotensinogen; angiotensin I; angiotensin II;
KW   analogue; blood flow; ischemic tissue; angiogenesis; cardiac remodelling;
KW   congestive heart disease; ischemic myocardial infarction;
KW   embyronic development; wound healing; chronic inflammatory disease.
XX
OS   Synthetic.
XX
PN   WO200009144-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US18374.
XX
PR   13-AUG-1998;   98US-0096414.
PR   18-SEP-1998;   98US-0101024.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-237409/20.
XX
PT   Increasing blood flow to ischemic tissue for minimizing cardiac
PT   remodelling and development of congestive heart failure involves
PT   administration of an active agent  -
XX
PS   Claim 2; Page 43; 56pp; English.
XX
CC   The present sequence represents an angiotensin II fragment. The
CC   specification also describes peptides derived from angiotensinogen,
CC   angiotensin I, angiotensin II, angiotensin III, and their analogues.
CC   The peptides are used for increasing blood flow to ischemic tissue.
CC   The peptides are angiogenesis stimulators. The peptides are useful for
CC   increasing blood flow to ischemic tissue by stimulating angiogenesis,
CC   and minimizing cardiac remodelling and development of congestive heart
CC   disease following a ischemic myocardial infarction. The stimulation of
CC   angiogenesis is also useful for embyronic development, wound healing
CC   and treating chronic inflammatory disease.
XX
SQ   Sequence   3 AA;


  Query Match           100.0%;  Score 15;  DB 21;  Length 3;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 drv 3
```

```
RESULT   6
AAR95671
ID   AAR95671 standard; peptide; 4 AA.
XX
AC   AAR95671;
XX
DT   09-JAN-1997  (first entry)
XX
DE   Angiotensin II fragment AII(1-4).
XX
KW   Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW   angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW   ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS   Synthetic.
XX
PN   WO9614858-A1.
XX
PD   23-MAY-1996.
XX
PF   14-NOV-1995;   95WO-US14764.
XX
PR   06-JUN-1995;   95US-0465775.
PR   14-NOV-1994;   94US-0337781.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Dizerega GS,  Rodgers K;
XX
DR   WPI; 1996-259561/26.
XX
PT   Accelerating wound healing by application of angiotensin II
PT   fragments  - are effective at very low concn. and do not cause
PT   hypertension
XX
PS   Disclosure; Page 4; 46pp; English.
XX
CC   AAR95663-R95672 represent fragments of angiotensin II (AT2).  AT2 (see
CC   AAR95662) is an octapeptide present in humans and other species.  AT2 is
CC   one of the most potent vasoconstrictors known, causing constriction of
CC   the arterioles.  The formation of angiotensin is initiated by the action
CC   of renin on angiotensinogen.  The substance formed is a decapeptide
CC   called angiotensin I which is converted by the enzyme angiotensinase (by
CC   removal of the C-terminal His-Leu) into AT2.  AT2 increases the release
CC   of extracellular matrices involved in wound repair.  These fragments can
CC   be used in a compound for accelerating wound healing.  The compounds are
CC   administered as matrical or micellar solutions, formulated with a
CC   carrier or diluent, alternatively the compound is applied in conjuncture
CC   with a wound dressing.  The carrier used in the composition is
CC   preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC   glycols.  By using fragments of this sequence (or analogues of it),
CC   growth as well as healing of tissues is improved, such as in cases of
CC   wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC   intraperitoneal surgical wounds.  The compounds containing the AT2
CC   fragments are less hypertensive than full length AT2, and are also
CC   effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 15;  DB 17;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 drv 3


RESULT   7
AAW64737
ID   AAW64737 standard; peptide; 4 AA.
XX
AC   AAW64737;
XX
DT   02-NOV-1998  (first entry)
XX
DE   Angiotensin II peptide #9.
XX
KW   Proliferation; mesenchymal stem cell; lineage-specific cell;
KW   haematopoietic; cell culture; transplantation; treatment; malignant;
KW   inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9832457-A2.
XX
PD   30-JUL-1998.
XX
PF   26-JAN-1998;   98WO-US01552.
XX
PR   23-JAN-1998;   98US-0066593.
PR   28-JAN-1997;   97US-0036507.
PR   08-MAY-1997;   97US-0046859.
PR   28-OCT-1997;   97US-0063684.
PR   31-OCT-1997;   97US-0063910.
PR   18-NOV-1997;   97US-0065612.
PR   26-NOV-1997;   97US-0066593.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   diZerega G,  Rodgers KE;
XX
DR   WPI; 1998-437044/37.
XX
PT   Promoting haematopoietic and mesenchymal cell proliferation and
PT   differentiation - by contacting the cells with angiotensinogen,
PT   angiotensin I or II, or analogues or fragments of these
XX
PS   Claim 7; Page 14; 114pp; English.
XX
CC   AAW64728-W64763 are peptides used in a novel method for accelerating the
CC   proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC   lineage-specific cells or mesenchymal lineage-specific cells. The method
CC   involves contacting the cells with an active agent comprising a sequence
CC   consisting of at least three contiguous amino acids of groups R1-R8 in
CC   the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC   form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC   Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC   carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC   azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC   6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC   not defined in the specification, the peptide bond between Ra and Rb is
CC   labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC   terminal Tyr group. A second active agent comprising a sequence
CC   consisting of at least three contiguous amino acids of groups R2-R8 in
CC   the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC   Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC   described. The inventions are particularly useful in cell culture
CC   mediums. These cells may be used in transplantation techniques for
CC   treatment of malignant or inherited diseases. The formulae represent
CC   analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC   or AII AT2 type 2 receptor agonists.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 15;  DB 19;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 drv 3
```

RESULT 8
AAW65606
ID AAW65606 standard; peptide; 4 AA.
XX
AC AAW65606;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-4).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 drv 3

RESULT 9
AAW71119
ID AAW71119 standard; peptide; 4 AA.
XX
AC AAW71119;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-4) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 drv 3

RESULT 10
AAW61302
ID AAW61302 standard; peptide; 4 AA.
XX
AC AAW61302;
XX
DT 02-OCT-1998 (first entry)
XX
DE Peptide 17 used to generate antibody.
XX
KW Immunosuppression; immunodeficiency; viral infection; neoplastic tissue;
KW cytokine imbalance; hormone imbalance; myalgic encephalomyelitis; ME;
KW viral infection fatigue syndrome; tuberculosis infection;
KW malarial infection; post inoculation fatigue syndrome.
XX
OS Synthetic.
XX
PN WO9810787-A2.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-IB01086.
XX
PR 11-SEP-1996; 96US-0025180.
XX
PA (PREN/) PRENDERGAST P T.

XX
PI Prendergast PT;
XX
DR WPI; 1998-271637/24.
XX
PT Immune system directed therapy - using specific amino acid sequences
PT exhibiting ion bridge pair arrays enclosed by hydrophobic segments
XX
PS Claim 95; Page 76; 83pp; English.
XX
CC The immunosuppressive amino acid sequences AAW61280-W61314 are used in
CC the method of the invention to enhance immune response in a patient
CC suffering from: (a) immunodeficiency resultant from (i) a viral
CC infection; (ii) bacterial, myocoplasmic, fungal and/or parasitic
CC infections; (iii) the growth of neoplastic tissue; (iv) any cytokine or
CC hormone imbalance or imbalance of any natural product within the
CC patient; (b) myalgic encephalomyelitis (ME); (c) post inoculation or
CC viral infection fatigue syndrome; (d) tuberculosis infection, and (e)
CC malarial infection.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 2 drv 4

RESULT 11
AAW61138
ID AAW61138 standard; peptide; 4 AA.
XX
AC AAW61138;
XX
DT 14-SEP-1998 (first entry)
XX
DE Peptide 17 used to produce antibodies against interleukin 10 mimic.
XX
KW Peptide; monoclonal; polyclonal; antibody; interleukin 10; IL10
KW alpha-fetoprotein; AFP; ion bridge pair array; infectious agent;
KW humoral; T cell; immune system; B cell; immunosuppression;
KW T helper cell; monocyte; cytotoxicity; IL2; gamma interferon; vaccine;
KW immunodeficiency; autoimmune disease; ss.
XX
OS Synthetic.
XX
PN WO9810792-A1.
XX
PD 19-MAR-1998.
XX
PF 13-SEP-1996; 96WO-IB00945.
XX
PR 11-SEP-1996; 96US-0025180.
XX
PA (PREN/) PRENDERGAST P T.
XX
PI Prendergast PT;
XX
DR WPI; 1998-260966/23.
XX
PT New immune system directed therapy - using specific amino acid
PT sequences which exhibit ion bridge pair arrays enclosed by a
PT non-polar hydrophobic segment
XX
PS Claim 8; Page 25; 31pp; English.
XX
CC The peptides AAW61122-W61148 can be used to raise monoclonal or
CC polyclonal antibodies (Ab) against an interleukin 10 (IL-10) or
CC alpha-fetoprotein (AFP) mimic. The peptides sequences contain ion bridge
CC pair arrays which are utilised in the infectious agents to enhance the
CC humoral Ab response and down regulate the T cell or delayed-type
CC hypersensitivity response. The peptides identified are used by infectious
CC agents to undermine the host's immune defence system and also to gain
CC entry to the target lymphoid tissue. This is caused by the non-specific
CC polyclonal B cell activation and immunosuppression. The mimic molecules
CC shut down the required Th1 T cell response which is needed to clear the
CC intracellular infections. Due to this, not enough immune reactive
CC monocytes are produced to overcome the initial infection. Upon
CC administration of the Ab, there will be an immediate Ab-dependent,
CC cell-mediated cytotoxicity-stimulated reduction in viral load, due to the
CC reduction of the IL-10/AFP mimic. Due to the presence of the Ab in the
CC hosts, the IL-10 and AFP mimics are no longer invisible and the Th1
CC response can be initiated, causing the synthesis of IL-2 and
CC gamma-interferon. The peptides can be used in the production of a
CC vaccine for the treatment of immunodeficiency, autoimmune disease,
CC infections, immune system disorders, etc.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 2 drv 4

RESULT 12
AAW47218
ID AAW47218 standard; peptide; 4 AA.
XX
AC AAW47218;
XX
DT 26-JUN-1998 (first entry)
XX
DE Variant MHC Class II DR beta-chain beta 1 domain residues 75-78.
XX
KW Determination; susceptibility; resistance; bovine leukaemia;
KW bovine leukaemia virus; BLV; beta 1 domain; bovine; MHC Class II;
KW DR beta-chain.
XX
OS Bos taurus.
XX
PN WO9803680-A1.
XX
PD 29-JAN-1998.
XX
PF 17-JUL-1997; 97WO-JP02485.
XX
PR 28-MAR-1997; 97JP-0077979.
PR 19-JUL-1996; 96JP-0190933.
XX
PA (RIKA ) INST PHYSICAL & CHEM RES.
XX
PI Aida Y;
XX
DR WPI; 1998-120797/11.
XX
PT Detecting susceptibility or resistance to bovine leukaemia caused by
PT bovine leukaemia virus - by detecting specific residues of the beta
PT 1 domain of bovine MHC Class II DR-beta chain; useful in cattle
PT farming
XX
PS Example 1; Page 11; 28pp; Japanese.
XX
CC The present sequence was used in the development of a novel method
CC to determine susceptibility, or resistance to bovine leukaemia
CC caused by bovine leukaemia virus (BLV). The method comprises
CC amplifying DNA encoding all or part of the beta 1 domain of the
CC bovine MHC Class II DR beta-chain from bovine genomic DNA,

CC expressing the DNA to give a beta 1 domain product and detecting
CC the amino acid sequence AAW47215, which is indicative of
CC susceptibility to bovine leukaemia caused by BLV, or Val78 in the
CC beta 1 domain which is indicative of resistance to bovine leukaemia
CC caused by BLV. Determination of the susceptibility or resistance to
CC bovine leukaemia caused by BLV is useful in dairy farming breeding
CC programs.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 2 drv 4

RESULT 13
AAY49595
ID AAY49595 standard; peptide; 4 AA.
XX
AC AAY49595;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:10.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 drv 3

RESULT 14
AAY33910
ID AAY33910 standard; peptide; 4 AA.
XX
AC AAY33910;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-4).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(1-4). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC or AII AT2 type 2 receptor agonists can rapidly provide a large
CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.
CC Similarly, methods that increase in vivo proliferation of ESCs will
CC enhance the utility of replacement therapy by rapidly increasing local
CC concentration of the stem cells and their progeny at the site of
CC therapy. The method also increases the potential utility of ESCs as
CC vehicles for gene therapy in certain disorders by more efficiently
CC providing a large number of such cells for transfection, and also by
CC providing a more efficient means to rapidly expand transfected ESCs.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRV 3
          |||
Db      1 drv 3


RESULT  15
AAY30548
ID   AAY30548 standard; peptide; 4 AA.
XX
AC   AAY30548;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII1-4.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents
XX
PS   Claim 2; Page 57; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   4 AA;


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  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
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Qy      1 DRV 3
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Db      1 drv 3


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Job time: 348 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:43:01 ; Search time 59.1 Seconds
(without alignments)
1.240 Million cell updates/sec

Title: US-09-723-197-11
Perfect score: 15
Sequence: 1 DRV 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 15 | 100.0 | 3 | 3 | US-09-208-337-11 | Sequence 11, Appl |
| 3 | 15 | 100.0 | 3 | 3 | US-08-990-664-12 | Sequence 12, Appl |
| 4 | 15 | 100.0 | 3 | 4 | US-09-373-962-11 | Sequence 11, Appl |
| 5 | 15 | 100.0 | 3 | 4 | US-09-245-680-11 | Sequence 11, Appl |
| 6 | 15 | 100.0 | 3 | 4 | US-09-198-806C-11 | Sequence 11, Appl |
| 7 | 15 | 100.0 | 3 | 4 | US-09-352-191-11 | Sequence 11, Appl |
| 8 | 15 | 100.0 | 3 | 4 | US-09-012-400-11 | Sequence 11, Appl |
| 9 | 15 | 100.0 | 4 | 2 | US-08-465-775-10 | Sequence 10, Appl |
| 10 | 15 | 100.0 | 4 | 3 | US-09-147-550-113 | Sequence 113, App |
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| 13 | 15 | 100.0 | 4 | 4 | US-09-373-962-10 | Sequence 10, Appl |
| 14 | 15 | 100.0 | 4 | 4 | US-09-245-680-10 | Sequence 10, Appl |
| 15 | 15 | 100.0 | 4 | 4 | US-09-198-806C-10 | Sequence 10, Appl |
| 16 | 15 | 100.0 | 4 | 4 | US-09-352-191-10 | Sequence 10, Appl |
| 17 | 15 | 100.0 | 4 | 4 | US-09-557-917-113 | Sequence 113, App |
| 18 | 15 | 100.0 | 4 | 4 | US-09-012-400-10 | Sequence 10, Appl |
| 19 | 15 | 100.0 | 5 | 2 | US-08-465-775-9 | Sequence 9, Appli |
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| 25 | 15 | 100.0 | 5 | 4 | US-09-245-680-9 | Sequence 9, Appli |
| 26 | 15 | 100.0 | 5 | 4 | US-09-198-806C-9 | Sequence 9, Appli |
| 27 | 15 | 100.0 | 5 | 4 | US-09-352-191-9 | Sequence 9, Appli |
| 28 | 15 | 100.0 | 5 | 4 | US-09-012-400-9 | Sequence 9, Appli |
| 29 | 15 | 100.0 | 5 | 5 | PCT-US95-02373-2 | Sequence 2, Appli |
| 30 | 15 | 100.0 | 6 | 2 | US-08-465-775-8 | Sequence 8, Appli |
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| 33 | 15 | 100.0 | 6 | 4 | US-09-373-962-8 | Sequence 8, Appli |
| 34 | 15 | 100.0 | 6 | 4 | US-09-245-680-8 | Sequence 8, Appli |
| 35 | 15 | 100.0 | 6 | 4 | US-09-198-806C-8 | Sequence 8, Appli |
| 36 | 15 | 100.0 | 6 | 4 | US-09-352-191-8 | Sequence 8, Appli |
| 37 | 15 | 100.0 | 6 | 4 | US-09-012-400-8 | Sequence 8, Appli |
| 38 | 15 | 100.0 | 7 | 1 | US-07-803-623B-16 | Sequence 16, Appl |
| 39 | 15 | 100.0 | 7 | 2 | US-08-806-084-16 | Sequence 16, Appl |
| 40 | 15 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 41 | 15 | 100.0 | 7 | 2 | US-09-047-594-1 | Sequence 1, Appli |
| 42 | 15 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 43 | 15 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
| 44 | 15 | 100.0 | 7 | 4 | US-09-371-710-19 | Sequence 19, Appl |
| 45 | 15 | 100.0 | 7 | 4 | US-09-373-962-4 | Sequence 4, Appli |

ALIGNMENTS

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US-08-465-775-11
; Sequence 11, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-11


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Qy       1 DRV 3
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Db       1 DRV 3
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US-09-208-337-11
; Sequence 11, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-11


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Db      1 DRV 3


RESULT   3
US-08-990-664-12
; Sequence 12, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
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;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-12


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Db      1 DRV 3


RESULT   4
US-09-373-962-11
; Sequence 11, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-3)
US-09-373-962-11


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Db      1 DRV 3
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; Sequence 11, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
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US-09-245-680-11


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Qy      1 DRV 3
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; Sequence 11, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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Qy      1 DRV 3
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Db      1 DRV 3


RESULT   7
US-09-352-191-11
; Sequence 11, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
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Db      1 DRV 3


RESULT   8
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; Sequence 11, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
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; SEQ ID NO 11
;   LENGTH: 3
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;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-3)
US-09-012-400-11


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Qy      1 DRV 3
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Db      1 DRV 3


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; Patent No. 5955430
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;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
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;    COMPUTER READABLE FORM:
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-10


  Query Match             100.0%;  Score 15;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT  10
US-09-147-550-113
; Sequence 113, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
;  APPLICANT: Aida, Yoko
;  TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
;  TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
;  FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
;  CURRENT APPLICATION NUMBER: US/09/147,550
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: PCT/JP97/02485
;  EARLIER FILING DATE: 1997-07-17
;  EARLIER APPLICATION NUMBER: JP 8-190933
;  EARLIER FILING DATE: 1996-07-19
;  EARLIER APPLICATION NUMBER: JP 9-77979
;  EARLIER FILING DATE: 1997-03-28
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: BOVINE
US-09-147-550-113


  Query Match             100.0%;  Score 15;  DB 3;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
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Db      2 DRV 4


RESULT  11
US-09-208-337-10
; Sequence 10, Application US/09208337
; Patent No. 6096709
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; GENERAL INFORMATION:
;   APPLICANT:  Rodgers, Kathleen
;   APPLICANT:  Gere, diZerega
;   TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;   TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;   NUMBER OF SEQUENCES:  15
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Knobbe, Martens, Olson & Bear
;     STREET:  620 Newport Center Drive  16th Floor
;     CITY:  Newport Beach
;     STATE:  CA
;     COUNTRY:  U.S.A.
;     ZIP:  92660
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/208,337
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/465,775
;     FILING DATE:  06-JUN-1995
;     APPLICATION NUMBER:  08/337,781
;     FILING DATE:  14-NOV-1994
;     APPLICATION NUMBER:  08/126,368
;     FILING DATE:  24-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Altman, Daniel E
;     REGISTRATION NUMBER:  34,115
;     REFERENCE/DOCKET NUMBER:  USC010.001CP2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  949-760-0404
;     TELEFAX:  949-760-9502
;     TELEX:
; INFORMATION FOR SEQ ID NO:  10:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  4 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  Peptide
US-09-208-337-10


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Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT  12
US-08-990-664-11
; Sequence 11, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;   APPLICANT:  Rodgers, Kathleen
;   APPLICANT:  diZerega, Gere
;   TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;   TITLE OF INVENTION:  IN SKIN GRAFTS
;   NUMBER OF SEQUENCES:  46
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Knobbe, Martens, Olson & Bear
;     STREET:  620 Newport Center Drive  16th Floor
;     CITY:  Newport Beach
;     STATE:  CA
;     COUNTRY:  U.S.A.
;     ZIP:  92660
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-11


  Query Match             100.0%;  Score 15;  DB 3;  Length 4;
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  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT  13
US-09-373-962-10
; Sequence 10, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-373-962-10


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Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT  14
US-09-245-680-10
; Sequence 10, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
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;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-245-680-10


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Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT  15
US-09-198-806C-10
; Sequence 10, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-4)
US-09-198-806C-10


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  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


Search completed: July  1, 2002, 07:43:01
Job time: 302 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 07:46:31 ; Search time 69.93 Seconds
(without alignments)
4.122 Million cell updates/sec

Title: US-09-723-197-11
Perfect score: 15
Sequence: 1 DRV 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 15 | 100.0 | 10 | 2 | A60624 | angiotensin I - Ja |
| 2 | 15 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 3 | 15 | 100.0 | 10 | 2 | A90917 | angiotensin precur |
| 4 | 15 | 100.0 | 10 | 2 | A90345 | angiotensin precur |
| 5 | 15 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 6 | 15 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 7 | 15 | 100.0 | 15 | 2 | PA0041 | plastoquinol--plas |
| 8 | 15 | 100.0 | 18 | 2 | H75063 | hypothetical prote |
| 9 | 15 | 100.0 | 20 | 2 | A31049 | calsequestrin, fas |
| 10 | 15 | 100.0 | 20 | 2 | A05313 | apolipoprotein A-I |
| 11 | 15 | 100.0 | 20 | 2 | S03987 | agglutinin beta-2 |
| 12 | 15 | 100.0 | 21 | 2 | S03986 | agglutinin beta-1 |
| 13 | 15 | 100.0 | 23 | 2 | B39313 | chaperonin, 10K - |
| 14 | 15 | 100.0 | 23 | 2 | C49732 | NADH dehydrogenase |
| 15 | 15 | 100.0 | 25 | 2 | A60502 | myonexin - norther |
| 16 | 15 | 100.0 | 28 | 2 | S55729 | orotidine-5'-monop |
| 17 | 15 | 100.0 | 33 | 2 | A42592 | precorrin-6x reduc |
| 18 | 15 | 100.0 | 34 | 2 | S68084 | probable RNA-bindi |
| 19 | 15 | 100.0 | 35 | 2 | B84674 | hypothetical prote |
| 20 | 15 | 100.0 | 35 | 2 | D82137 | hypothetical prote |
| 21 | 15 | 100.0 | 36 | 2 | B82111 | hypothetical prote |
| 22 | 15 | 100.0 | 36 | 2 | A61235 | fibroblast-activat |
| 23 | 15 | 100.0 | 36 | 2 | A40723 | poly-Ig receptor - |
| 24 | 15 | 100.0 | 36 | 2 | B82827 | hypothetical prote |
| 25 | 15 | 100.0 | 37 | 2 | B85574 | hypothetical prote |
| 26 | 15 | 100.0 | 38 | 2 | A60216 | hyperglycemic horm |
| 27 | 15 | 100.0 | 38 | 2 | S78357 | photosystem II pro |
| 28 | 15 | 100.0 | 38 | 2 | H82780 | hypothetical prote |
| 29 | 15 | 100.0 | 38 | 2 | E89922 | hypothetical prote |
| 30 | 15 | 100.0 | 39 | 2 | E69677 | phosphatase (RapI) |
| 31 | 15 | 100.0 | 40 | 2 | B27740 | gas-vesicle protei |
| 32 | 15 | 100.0 | 40 | 2 | I41476 | probable antigen 9 |
| 33 | 15 | 100.0 | 40 | 2 | T07583 | hypothetical prote |
| 34 | 15 | 100.0 | 40 | 2 | T07574 | hypothetical prote |
| 35 | 15 | 100.0 | 40 | 2 | A82529 | hypothetical prote |
| 36 | 15 | 100.0 | 41 | 1 | TITZ | trypsin inhibitor |
| 37 | 15 | 100.0 | 41 | 2 | S77772 | ribose-phosphate p |
| 38 | 15 | 100.0 | 42 | 2 | I65746 | tropomyosin - huma |
| 39 | 15 | 100.0 | 43 | 2 | S42852 | melA protein - Sal |
| 40 | 15 | 100.0 | 44 | 2 | F81839 | hypothetical prote |
| 41 | 15 | 100.0 | 45 | 2 | D82399 | hypothetical prote |
| 42 | 15 | 100.0 | 46 | 2 | PC4400 | crotoxin-binding p |
| 43 | 15 | 100.0 | 47 | 2 | S78708 | protein YBR126w-a |
| 44 | 15 | 100.0 | 48 | 2 | S19612 | chlorophyll a/b-bi |
| 45 | 15 | 100.0 | 50 | 2 | H90760 | hypothetical prote |

ALIGNMENTS

RESULT 1
A60624
angiotensin I - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of t
A;Reference number: A60624; MUID:90284684
A;Accession: A60624
A;Molecule type: protein
A;Residues: 1-10 <TAK>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
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Db 1 DRV 3

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S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 15; DB 2; Length 10;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 DRV 3

RESULT 3
A90917
angiotensin precursor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90917; A01250
R;Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A;Reference number: A90917; MUID:74127845
A;Accession: A90917
A;Molecule type: protein
A;Residues: 1-10 <NAK>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 DRV 3

RESULT 4
A90345
angiotensin precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90345; A01250
R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 DRV 3

RESULT 5
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
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F;1-8/Product: angiotensin II #status experimental <AN2>

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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 DRV 3

RESULT 6
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 1 DRV 3

RESULT 7
PA0041
plastoquinol--plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PA0041
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A;Reference number: PA0001
A;Accession: PA0041
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: leaf
C;Keywords: oxidoreductase

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 7 DRV 9

RESULT 8
H75063
hypothetical protein PAB7382 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H75063
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A;Reference number: A75001

A;Accession: H75063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50405.1; PID:e151630
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB7382

Query Match 100.0%; Score 15; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 11 DRV 13

RESULT 9
A31049
calsequestrin, fast skeletal muscle - rat (fragment)
N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Jul-1999
C;Accession: A31049; S46193; S46194; S46195
R;Hall, D.E.; Frazer, K.A.; Hann, B.C.; Reichardt, L.F.
J. Cell Biol. 107, 687-697, 1988
A;Title: Isolation and characterization of a laminin-binding protein from rat and chick
A;Reference number: A92751; MUID:88331073
A;Accession: A31049
A;Molecule type: protein
A;Residues: 1-20 <HAL>
R;Volpe, P.; Martini, A.; Furlan, S.; Meldolesi, J.
Biochem. J. 301, 465-469, 1994
A;Title: Calsequestrin is a component of smooth muscles: the skeletal- and cardiac-muscl
A;Reference number: S46193; MUID:94318050
A;Accession: S46193
A;Molecule type: protein
A;Residues: 1-9 <VOL>
A;Accession: S46194
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'XXX',4-10,'X',12 <VO2>
A;Accession: S46195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'XE',3-12 <VO3>
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c
C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi
C;Superfamily: calsequestrin
C;Keywords: calcium binding; glycoprotein; skeletal muscle

Query Match 100.0%; Score 15; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 13 DRV 15

RESULT 10
A05313
apolipoprotein A-I - red guenon (fragment)
N;Alternate names: apo-A-I
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-May-2000
C;Accession: A05313
R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythroce
A;Reference number: A90395; MUID:76184721
A;Accession: A05313
A;Molecule type: protein
A;Residues: 1-20 <MAH>
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; l

Query Match 100.0%; Score 15; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 9 DRV 11

RESULT 11
S03987
agglutinin beta-2 chain - Osage orange
C;Species: Maclura pomifera (Osage orange)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C;Accession: S03987
R;Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.
Arch. Biochem. Biophys. 270, 596-603, 1989
A;Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia an
A;Reference number: S03983; MUID:89206218
A;Accession: S03987
A;Molecule type: protein
A;Residues: 1-20 <YOU>

Query Match 100.0%; Score 15; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 16 DRV 18

RESULT 12
S03986
agglutinin beta-1 chain - Osage orange
C;Species: Maclura pomifera (Osage orange)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Aug-1997
C;Accession: S03986; S03988
R;Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.
Arch. Biochem. Biophys. 270, 596-603, 1989
A;Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia an
A;Reference number: S03983; MUID:89206218
A;Accession: S03986
A;Molecule type: protein
A;Residues: 1-21 <YOU>
A;Note: beta-1 form
A;Accession: S03988
A;Molecule type: protein
A;Residues: 2-21 <YO2>
A;Note: beta-3 form

Query Match 100.0%; Score 15; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 17 DRV 19

RESULT 13
B39313

chaperonin, 10K - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 16-Feb-1997
C;Accession: B39313
R;Taguchi, H.; Konishi, J.; Ishii, N.; Yoshida, M.
J. Biol. Chem. 266, 22411-22418, 1991
A;Title: A chaperonin from a thermophilic bacterium, Thermus thermophilus, that controls
A;Reference number: A39313; MUID:92042183
A;Accession: B39313
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-23 <TAG>
C;Keywords: molecular chaperone

Query Match 100.0%; Score 15; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 13 DRV 15

RESULT 14
C49732
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 29K chain - potato mitochondrion (fragment)
N;Alternate names: complex 1 dehydrogenase 29K chain; NADH-ubiquinone oxidoreductase 29K
C;Species: mitochondrion Solanum tuberosum (potato)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C;Accession: C49732
R;Herz, U.; Schroeder, W.; Liddell, A.; Leaver, C.J.; Brennicke, A.; Grohmann, L.
J. Biol. Chem. 269, 2263-2269, 1994
A;Title: Purification of the NADH:ubiquinone oxidoreductase (complex I) of the respirato
A;Reference number: A49732; MUID:94124587
A;Accession: C49732
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-23 <HER>
C;Genetics:
A;Genome: mitochondrion
C;Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane; mit

Query Match 100.0%; Score 15; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 13 DRV 15

RESULT 15
A60502
myonexin - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: A60502; A33087
R;Tidball, J.G.
Dev. Biol. 142, 103-114, 1990
A;Title: Myonexin: an 80-kDa glycoprotein that binds fibronectin and is located at embry
A;Reference number: A60502; MUID:91032554
A;Accession: A60502
A;Molecule type: protein
A;Residues: 1-25 <TID>
C;Comment: This protein resembles calsequestrin in sequence but differs in distribution
C;Superfamily: calsequestrin
C;Keywords: fibronectin binding; glycoprotein; skeletal muscle

Query Match 100.0%; Score 15; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 13 DRV 15

Search completed: July 1, 2002, 07:46:32
Job time: 453 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:47:10 ; Search time 34.05 Seconds
(without alignments)
3.411 Million cell updates/sec

Title: US-09-723-197-11
Perfect score: 15
Sequence: 1 DRV 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 15 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 15 | 100.0 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 3 | 15 | 100.0 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 4 | 15 | 100.0 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 5 | 15 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 6 | 15 | 100.0 | 19 | 1 | FIBB_LAMGL | P14473 lama glama |
| 7 | 15 | 100.0 | 20 | 1 | APA1_ERYPA | P18647 erythrocebu |
| 8 | 15 | 100.0 | 20 | 1 | CAQS_RAT | P19633 rattus norv |
| 9 | 15 | 100.0 | 20 | 1 | LEC2_MACPO | P18676 maclura pom |
| 10 | 15 | 100.0 | 20 | 1 | LEC3_MACPO | P18677 maclura pom |
| 11 | 15 | 100.0 | 20 | 1 | PGK_BACCE | P83075 bacillus ce |
| 12 | 15 | 100.0 | 21 | 1 | CH1C_PEA | P31233 pisum sativ |
| 13 | 15 | 100.0 | 21 | 1 | LEC1_MACPO | P18675 maclura pom |
| 14 | 15 | 100.0 | 23 | 1 | NUO5_SOLTU | P80262 solanum tub |
| 15 | 15 | 100.0 | 26 | 1 | AMD1_CHICK | P81073 gallus gall |
| 16 | 15 | 100.0 | 26 | 1 | AMD1_RABIT | P81072 oryctolagus |
| 17 | 15 | 100.0 | 38 | 1 | PSBX_ODOSI | P49509 odontella s |
| 18 | 15 | 100.0 | 39 | 1 | PSBX_GUITH | O78455 guillardia |
| 19 | 15 | 100.0 | 41 | 1 | ITRY_TRIKI | P01069 trichosanth |
| 20 | 15 | 100.0 | 43 | 1 | VPU_HV1C4 | P08803 human immun |
| 21 | 15 | 100.0 | 49 | 1 | R331_BACSU | P56849 bacillus su |
| 22 | 15 | 100.0 | 54 | 1 | VPW_BIV27 | P24034 bovine immu |
| 23 | 15 | 100.0 | 55 | 1 | RMF_ECOLI | P22986 escherichia |
| 24 | 15 | 100.0 | 56 | 1 | CAQS_CANFA | P31236 canis famil |
| 25 | 15 | 100.0 | 57 | 1 | Y160_ARCFU | O28419 archaeoglob |
| 26 | 15 | 100.0 | 58 | 1 | ACEA_HELAN | P20699 helianthus |
| 27 | 15 | 100.0 | 61 | 1 | PPSA_ERWHE | O54457 erwinia her |
| 28 | 15 | 100.0 | 62 | 1 | DSRB_ECOLI | P40678 escherichia |
| 29 | 15 | 100.0 | 63 | 1 | YOR4_TTV1 | P19279 thermoprote |
| 30 | 15 | 100.0 | 64 | 1 | SCX5_ANDMA | P01482 androctonus |
| 31 | 15 | 100.0 | 64 | 1 | SCX5_LEIQU | P01481 leiurus qui |
| 32 | 15 | 100.0 | 65 | 1 | RL35_BUCAI | P57227 buchnera ap |
| 33 | 15 | 100.0 | 65 | 1 | SCX3_MESMA | P15227 mesobuthus |
| 34 | 15 | 100.0 | 66 | 1 | Y13G_BPT4 | P39500 bacteriopha |
| 35 | 15 | 100.0 | 67 | 1 | CSPA_MICLU | O30875 micrococcus |
| 36 | 15 | 100.0 | 67 | 1 | SCX3_ORTSC | P15225 orthochirus |
| 37 | 15 | 100.0 | 67 | 1 | YPUB_BACSU | P35151 bacillus su |
| 38 | 15 | 100.0 | 68 | 1 | BGIA_MOMCH | P24076 momordica c |
| 39 | 15 | 100.0 | 69 | 1 | ACP_RHOSH | P12784 rhodobacter |
| 40 | 15 | 100.0 | 69 | 1 | ATSI_AMACA | P80211 amaranthus |
| 41 | 15 | 100.0 | 69 | 1 | ICI_LINUS | P82381 linum usita |
| 42 | 15 | 100.0 | 70 | 1 | FLC1_ECOLI | P11519 escherichia |
| 43 | 15 | 100.0 | 70 | 1 | FLC2_ECOLI | P23587 escherichia |
| 44 | 15 | 100.0 | 70 | 1 | Y4ON_RHISN | P55599 rhizobium s |
| 45 | 15 | 100.0 | 71 | 1 | CHH1_MACRS | P81206 macrobrachi |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRV 3
          |||
Db      1 DRV 3
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RESULT 2
ANG1_BOTJA
ID ANG1_BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

```
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1308 MW;  CEF50DD761F2DB42 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   3
ANGT_BOVIN
ID   ANGT_BOVIN     STANDARD;      PRT;    10 AA.
AC   P01017;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RA   Elliott D.F., Peart W.S.;
RT   "The amino acid sequence in a hypertensin.";
RL   Biochem. J. 65:246-254(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90345; A90345.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1282 MW;  CEEFBDD761F2DB42 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   4
ANGT_CHICK
ID   ANGT_CHICK     STANDARD;      PRT;    10 AA.
AC   P01018;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken;
RX   MEDLINE=74127845; PubMed=4361802;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. 3. Structure of fowl
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 21:2085-2087(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=90284684; PubMed=2191893;
RA   Takei Y., Hasegawa Y.;
RT   "Vasopressor and depressor effects of native angiotensins and
RT   inhibition of these effects in the Japanese quail.";
RL   Gen. Comp. Endocrinol. 79:12-22(1990).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90917; A90917.
DR   PIR; A60624; A60624.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1232 MW;  CEFBEDD761F2DB42 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   5
ANGT_HORSE
ID   ANGT_HORSE     STANDARD;      PRT;    14 AA.
AC   P01016;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE.
RA   Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT   "The preparation, purification, and amino acid sequence of a
RT   polypeptide renin substrate.";
RL   J. Exp. Med. 106:439-453(1957).
```

```
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   6
FIBB_LAMGL
ID   FIBB_LAMGL     STANDARD;      PRT;    19 AA.
AC   P14473;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN   FGB.
OS   Lama glama (Llama),
OS   Lama vicugna (Vicugna) (Vicugna vicugna), and
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844, 9843, 9838;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=L.glama;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.dromedarius;
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.vicugna;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC       POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC       AGGREGATION.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC       THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC       CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Plasma; Sulfation.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE B.
FT   MOD_RES       4      4       SULFATION.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2295 MW;  E7EE6B6100568638 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     10 DRV 12


RESULT   7
APA1_ERYPA
ID   APA1_ERYPA     STANDARD;      PRT;    20 AA.
AC   P18647;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Apolipoprotein A-I (Apo-AI) (Fragment).
GN   APOA1.
OS   Erythrocebus patas (Red guenon) (Hussar).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Erythrocebus.
OX   NCBI_TaxID=9538;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76184721; PubMed=178359;
RA   Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT   "Characterization of the plasma lipoproteins and apoproteins of the
RT   Erythrocebus patas monkey.";
RL   Biochemistry 15:1928-1933(1976).
CC   -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC       CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC       CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC       THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC       CHYLOMICRONS.
CC   -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR   PIR; A05313; A05313.
KW   Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2387 MW;  9C970997C7FC976A CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      9 DRV 11


RESULT   8
CAQS_RAT
ID   CAQS_RAT       STANDARD;      PRT;    20 AA.
AC   P19633;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Calsequestrin, skeletal muscle isoform (Aspartactin) (Laminin-binding
DE   protein) (Fragment).
GN   CASQ1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=88331073; PubMed=3417768;
RA   Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;
RT   "Isolation and characterization of a laminin-binding protein from rat
RT   and chick muscle.";
RL   J. Cell Biol. 107:687-697(1988).
CC   -!- FUNCTION: CALSEQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,
CC       CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE
CC       IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTRIN THROUGH
CC       A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
CC       TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
CC   -!- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTRIN OCCURS IN THE
CC       SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF
CC       FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL
CC       LAMINA SURROUNDING INDIVIDUAL MUSCLE FIBERS.
CC   -!- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE CALSEQUESTRIN FAMILY.
DR   PIR; A31049; A31049.
DR   HSSP; P07221; 1A8Y.
DR   InterPro; IPR001393; Calsequestrin.
DR   PROSITE; PS00864; CALSEQUESTRIN_2; PARTIAL.
DR   PROSITE; PS00863; CALSEQUESTRIN_1; 1.
KW   Muscle; Glycoprotein; Calcium-binding.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2238 MW;  92ADE04FC2A69280 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRV 3
           |||
Db      13 DRV 15


RESULT   9
LEC2_MACPO
ID   LEC2_MACPO     STANDARD;      PRT;    20 AA.
AC   P18676;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   Agglutinin beta-2 chain (MPA).
OS   Maclura pomifera (Osage orange).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Rosales; Moraceae; Maclura.
OX   NCBI_TaxID=3496;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Seed;
RX   MEDLINE=89206218; PubMed=2705782;
RA   Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT   "Homology of the D-galactose-specific lectins from Artocarpus
RT   integrifolia and Maclura pomifera and the role of an unusual small
RT   polypeptide subunit.";
RL   Arch. Biochem. Biophys. 270:596-603(1989).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=98165814; PubMed=9497359;
RA   Lee X., Thompson A., Zhang Z., Ton-That H., Biesterfeldt J., Ogata C.,
RA   Xu L., Johnston R.A., Young N.M.;
RT   "Structure of the complex of Maclura pomifera agglutinin and the T-
RT   antigen disaccharide, Galbeta1,3GalNAc.";
RL   J. Biol. Chem. 273:6312-6318(1998).
CC   -!- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC       STRUCTURE GAL-BETA1-3-GALNAC.
CC   -!- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC   -!- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR   PIR; S03987; S03987.
DR   PDB; 1JOT; 16-FEB-99.
KW   Lectin; 3D-structure.
SQ   SEQUENCE   20 AA;  2141 MW;  AA3882AD5D6370E0 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRV 3
           |||
Db      16 DRV 18


RESULT   10
LEC3_MACPO
ID   LEC3_MACPO     STANDARD;      PRT;    20 AA.
AC   P18677;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   Agglutinin beta-3 chain (MPA).
OS   Maclura pomifera (Osage orange).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Rosales; Moraceae; Maclura.
OX   NCBI_TaxID=3496;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Seed;
RX   MEDLINE=89206218; PubMed=2705782;
RA   Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT   "Homology of the D-galactose-specific lectins from Artocarpus
RT   integrifolia and Maclura pomifera and the role of an unusual small
RT   polypeptide subunit.";
RL   Arch. Biochem. Biophys. 270:596-603(1989).
CC   -!- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC       STRUCTURE GAL-BETA1-3-GALNAC.
CC   -!- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC   -!- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR   PIR; S03988; S03988.
DR   HSSP; P18676; 1JOT.
KW   Lectin.
SQ   SEQUENCE   20 AA;  2082 MW;  AA38811BBD6370E0 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRV 3
           |||
Db      16 DRV 18


RESULT   11
PGK_BACCE
ID   PGK_BACCE      STANDARD;      PRT;    20 AA.
AC   P83075;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).
OS   Bacillus cereus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1396;
RN   [1]
RP   SEQUENCE, AND INDUCTION.
RC   STRAIN=NCIMB 11796;
RA   Browne N., Dowds B.C.A.;
RL   Submitted (JUL-2001) to the SWISS-PROT data bank.
CC   -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
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CC       phospho-D-glyceroyl phosphate.
CC   -!- PATHWAY: Second step in the second phase of glycolysis.
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- INDUCTION: By heat shock.
CC   -!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DR   InterPro; IPR001576; PGK.
DR   PROSITE; PS00111; PGLYCERATE_KINASE; PARTIAL.
KW   Transferase; Kinase; Glycolysis; Heat shock.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2403 MW;  EDAD2CAF1155C353 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     18 DRV 20


RESULT  12
CH1C_PEA
ID   CH1C_PEA       STANDARD;      PRT;    21 AA.
AC   P31233;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   20 kDa chaperonin, chloroplast (Protein Cpn21) (Chloroplast protein
DE   Cpn10) (Chloroplast chaperonin 10) (Ch-CPN10) (Fragment).
GN   CPN21 OR CHCPN10.
OS   Pisum sativum (Garden pea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX   NCBI_TaxID=3888;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92409583; PubMed=1356267;
RA   Bertsch U., Soll J., Seetharam R., Viitanen P.V.;
RT   "Identification, characterization, and DNA sequence of a functional
RT   'double' groES-like chaperonin from chloroplasts of higher plants.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8696-8700(1992).
CC   -!- FUNCTION: SEEMS TO FUNCTION ONLY AS A COCHAPERONIN, ALONG WITH
CC       CPN60, AND IN CERTAIN CASES IS ESSENTIAL FOR THE DISCHARGE OF
CC       BIOLOGICALLY ACTIVE PROTEINS FROM CPN60.
CC   -!- SUBUNIT: FORMS STABLE COMPLEXES WITH CPN60 IN THE PRESENCE
CC       OF ATP.
CC   -!- SUBCELLULAR LOCATION: Chloroplast.
CC   -!- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
DR   InterPro; IPR001476; Cpn10.
DR   Pfam; PF00166; cpn10; 1.
DR   PROSITE; PS00681; CHAPERONINS_CPN10; PARTIAL.
KW   Chaperone; Chloroplast.
FT   NON_TER      21     21
SQ   SEQUENCE   21 AA;  2240 MW;  260295B3C087FD95 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     16 DRV 18


RESULT  13
LEC1_MACPO
ID   LEC1_MACPO     STANDARD;      PRT;    21 AA.
AC   P18675;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   Agglutinin beta-1 chain (MPA).
OS   Maclura pomifera (Osage orange).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Rosales; Moraceae; Maclura.
OX   NCBI_TaxID=3496;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Seed;
RX   MEDLINE=89206218; PubMed=2705782;
RA   Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT   "Homology of the D-galactose-specific lectins from Artocarpus
RT   integrifolia and Maclura pomifera and the role of an unusual small
RT   polypeptide subunit.";
RL   Arch. Biochem. Biophys. 270:596-603(1989).
CC   -!- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC       STRUCTURE GAL-BETA1-3-GALNAC.
CC   -!- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC   -!- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR   PIR; S03986; S03986.
DR   HSSP; P18676; 1JOT.
KW   Lectin.
SQ   SEQUENCE   21 AA;  2196 MW;  AA38811BC1BFD0E0 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     17 DRV 19


RESULT  14
NUO5_SOLTU
ID   NUO5_SOLTU     STANDARD;      PRT;    23 AA.
AC   P80262;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   NADH-ubiquinone oxidoreductase 29 kDa subunit (EC 1.6.5.3)
DE   (EC 1.6.99.3) (Complex I-29KD) (CI-29KD) (Fragment).
OS   Solanum tuberosum (Potato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4113;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. BINTJE; TISSUE=Tuber;
RX   MEDLINE=94124587; PubMed=8294484;
RA   Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
RA   Grohmann L.;
RT   "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
RT   the respiratory chain from the inner mitochondrial membrane of
RT   Solanum tuberosum.";
RL   J. Biol. Chem. 269:2263-2269(1994).
CC   -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC       CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC       TO BE UBIQUINONE.
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
CC       MEMBRANE.
DR   PIR; C49732; C49732.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2653 MW;  4B41B8FF83412F58 CRC64;
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  Query Match             100.0%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRV 3
           |||
Db      13 DRV 15


RESULT  15
AMD1_CHICK
ID   AMD1_CHICK     STANDARD;      PRT;    26 AA.
AC   P81073;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase
DE   isoform M) (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Breast;
RX   MEDLINE=97269365; PubMed=9114497;
RA   Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RT   "AMP-deaminases from chicken and rabbit muscle: partial primary
RT   sequences of homologous 17-kDa CNBr fragments: autorecognition by
RT   rabbit anti-[chicken AMPD].";
RL   Comp. Biochem. Physiol. 116B:371-377(1997).
CC   -!- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY
CC       METABOLISM.
CC   -!- CATALYTIC ACTIVITY: AMP + H(2)O = IMP + NH(3).
CC   -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
DR   InterPro; IPR001365; A_deaminase.
DR   PROSITE; PS00485; A_DEAMINASE; PARTIAL.
KW   Hydrolase; Nucleotide metabolism; Multigene family.
FT   NON_TER       1      1
FT   NON_TER      26     26
SQ   SEQUENCE   26 AA;  3195 MW;  B03E296D63BB6E75 CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRV 3
           |||
Db      19 DRV 21


Search completed: July  1, 2002, 07:47:11
Job time: 477 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:45:16 ; Search time 122.73 Seconds
(without alignments)
4.229 Million cell updates/sec

Title: US-09-723-197-11
Perfect score: 15
Sequence: 1 DRV 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 15 | 100.0 | 9 | 12 | Q83622 | Q83622 murray vall |
| 2 | 15 | 100.0 | 10 | 13 | Q9PS07 | Q9ps07 alligator m |
| 3 | 15 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 4 | 15 | 100.0 | 15 | 2 | Q9R4K0 | Q9r4k0 nocardia. n |
| 5 | 15 | 100.0 | 15 | 2 | Q9R521 | Q9r521 francisella |
| 6 | 15 | 100.0 | 15 | 2 | O05991 | O05991 staphylococ |
| 7 | 15 | 100.0 | 16 | 1 | Q9UWJ4 | Q9uwj4 pyrococcus |
| 8 | 15 | 100.0 | 17 | 12 | O89807 | O89807 epiphyas po |
| 9 | 15 | 100.0 | 18 | 4 | Q9BU72 | Q9bu72 homo sapien |
| 10 | 15 | 100.0 | 18 | 17 | Q9UYK7 | Q9uyk7 pyrococcus |
| 11 | 15 | 100.0 | 19 | 10 | P83089 | P83089 spinacia ol |
| 12 | 15 | 100.0 | 19 | 11 | Q9Z1I5 | Q9z1i5 rattus sp. |
| 13 | 15 | 100.0 | 20 | 2 | Q9R519 | Q9r519 mycobacteri |
| 14 | 15 | 100.0 | 20 | 11 | Q9QVG0 | Q9qvg0 rattus sp. |
| 15 | 15 | 100.0 | 22 | 2 | Q47529 | Q47529 escherichia |
| 16 | 15 | 100.0 | 24 | 8 | Q9T2H3 | Q9t2h3 spinacia ol |
| 17 | 15 | 100.0 | 25 | 2 | Q51310 | Q51310 nostoc sp. |
| 18 | 15 | 100.0 | 26 | 4 | Q9UCT8 | Q9uct8 homo sapien |
| 19 | 15 | 100.0 | 27 | 12 | O56510 | O56510 hepatitis c |
| 20 | 15 | 100.0 | 28 | 4 | Q96F68 | Q96f68 homo sapien |
| 21 | 15 | 100.0 | 29 | 4 | Q9UEF0 | Q9uef0 homo sapien |
| 22 | 15 | 100.0 | 29 | 5 | Q9TX02 | Q9tx02 chironomus |
| 23 | 15 | 100.0 | 29 | 12 | Q919A6 | Q919a6 porcine rep |
| 24 | 15 | 100.0 | 31 | 11 | Q99PC8 | Q99pc8 rattus norv |
| 25 | 15 | 100.0 | 33 | 8 | Q9T2N1 | Q9t2n1 nicotiana t |
| 26 | 15 | 100.0 | 33 | 8 | Q9T2M1 | Q9t2m1 nicotiana t |
| 27 | 15 | 100.0 | 33 | 11 | Q62676 | Q62676 rattus norv |
| 28 | 15 | 100.0 | 35 | 10 | Q9FJ84 | Q9fj84 arabidopsis |
| 29 | 15 | 100.0 | 35 | 10 | Q9LV08 | Q9lv08 arabidopsis |
| 30 | 15 | 100.0 | 35 | 10 | Q9ZUW2 | Q9zuw2 arabidopsis |
| 31 | 15 | 100.0 | 35 | 13 | Q90XB5 | Q90xb5 xenopus lae |
| 32 | 15 | 100.0 | 35 | 16 | Q9KQQ2 | Q9kqq2 vibrio chol |
| 33 | 15 | 100.0 | 36 | 2 | O68947 | O68947 azomonas ma |
| 34 | 15 | 100.0 | 36 | 10 | Q42333 | Q42333 arabidopsis |
| 35 | 15 | 100.0 | 36 | 16 | Q9PGM9 | Q9pgm9 xylella fas |
| 36 | 15 | 100.0 | 36 | 16 | Q9KQ35 | Q9kq35 vibrio chol |
| 37 | 15 | 100.0 | 38 | 12 | Q9WNW6 | Q9wnw6 japanese en |
| 38 | 15 | 100.0 | 38 | 16 | Q9PFK7 | Q9pfk7 xylella fas |
| 39 | 15 | 100.0 | 38 | 16 | Q99U43 | Q99u43 staphylococ |
| 40 | 15 | 100.0 | 39 | 2 | Q9RIJ8 | Q9rij8 streptococc |
| 41 | 15 | 100.0 | 39 | 16 | O31492 | O31492 bacillus su |
| 42 | 15 | 100.0 | 40 | 2 | Q9KZ25 | Q9kz25 streptomyce |
| 43 | 15 | 100.0 | 40 | 7 | O62886 | O62886 canis famil |
| 44 | 15 | 100.0 | 40 | 8 | Q32999 | Q32999 pinus thunb |
| 45 | 15 | 100.0 | 40 | 8 | Q33006 | Q33006 pinus thunb |

ALIGNMENTS

RESULT 1
Q83622
ID Q83622 PRELIMINARY; PRT; 9 AA.
AC Q83622;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 1.1 KDA PROTEIN (FRAGMENT).
OS Murray valley encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11079;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118912; PubMed=2828633;
RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,
RA Strauss J.H.;
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs
RT and potential cyclization sequences.";
RL J. Mol. Biol. 198:33-41(1987).
DR EMBL; M35172; AAA66627.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;

Query Match 100.0%; Score 15; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 6 DRV 8

RESULT 2
Q9PS07
ID Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;

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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ANGIOTENSIN I, ANG I.
OS   Alligator mississippiensis (American alligator).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX   NCBI_TaxID=8496;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93307610; PubMed=8319878;
RA   Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA   Stephens G.A., Sakakibara S.;
RT   "New angiotensin I isolated from a reptile, Alligator
RT   mississippiensis.";
RL   Gen. Comp. Endocrinol. 90:214-219(1993).
SQ   SEQUENCE   10 AA;  1216 MW;  CEE38DD761F2DB42 CRC64;


  Query Match             100.0%;  Score 15;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   3
Q10757
ID   Q10757      PRELIMINARY;      PRT;    14 AA.
AC   Q10757;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
OS   Theromyzon tessulatum (Leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX   NCBI_TaxID=13286;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95365039; PubMed=7637887;
RA   Laurent V., Bulet P., Salzet M.A.;
RT   "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT   molecule with forms of vertebrate angiotensinogens: a hormonal system
RT   conserved in the course of evolution.";
RL   Neurosci. Lett. 190:175-178(1995).
RN   [2]
RP   SEQUENCE OF 1-10.
RC   TISSUE=BRAIN;
RX   MEDLINE=96201949; PubMed=8612806;
RA   Laurent V., Salzet M.;
RT   "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT   tessulatum.";
RL   FEBS Lett. 384:123-127(1996).
CC   -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW   Glycoprotein; Serpin.
FT   NON_TER      14      14
SQ   SEQUENCE   14 AA;  1763 MW;  335109D8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 15;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      1 DRV 3


RESULT   4
Q9R4K0
ID   Q9R4K0      PRELIMINARY;      PRT;    15 AA.
AC   Q9R4K0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   NITRIC OXIDE SYNTHASE (EC 4.14.23.-).
OS   Nocardia.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Nocardiaceae.
OX   NCBI_TaxID=1817;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95394819; PubMed=7545152;
RA   Chen Y., Rosazza J.P.;
RT   "Purification and characterization of nitric oxide synthase (NOSNoc)
RT   from a Nocardia species.";
RL   J. Bacteriol. 177:5122-5128(1995).
SQ   SEQUENCE   15 AA;  1818 MW;  2BD5B859DE288B77 CRC64;


  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     10 DRV 12


RESULT   5
Q9R521
ID   Q9R521      PRELIMINARY;      PRT;    15 AA.
AC   Q9R521;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   GROES HOMOLOG (FRAGMENT).
OS   Francisella tularensis.
OC   Bacteria; Proteobacteria; gamma subdivision; Francisella group;
OC   Francisella.
OX   NCBI_TaxID=263;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94086099; PubMed=7903283;
RA   Ericsson M., Tarnvik A., Kuoppa K., Sandstrom G., Sjostedt A.;
RT   "Increased synthesis of DnaK, GroEL, and GroES homologs by Francisella
RT   tularensis LVS in response to heat and hydrogen peroxide.";
RL   Infect. Immun. 62:178-183(1994).
DR   InterPro; IPR001476; Cpn10.
DR   Pfam; PF00166; cpn10; 1.
SQ   SEQUENCE   15 AA;  1837 MW;  9DCF2D4507437D33 CRC64;


  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      8 DRV 10


RESULT   6
O05991
ID   O05991      PRELIMINARY;      PRT;    15 AA.
AC   O05991;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   SIMILAR TO BIN3 AND SIN RECOMBINASES OF STAPHYLOCOCCUS AUREUS
DE   (FRAGMENT).
OS   Staphylococcus simulans.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
```

```
OC   Bacillus/Staphylococcus group; Staphylococcus.
OX   NCBI_TaxID=1286;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97260121; PubMed=9106216;
RA   Thumm G., Gotz F.;
RT   "Studies on prolysostaphin processing and characterization of the
RT   lysostaphin immunity factor (Lif) of Staphylococcus simulans biovar
RT   staphylolyticus.";
RL   Mol. Microbiol. 23:1251-1265(1997).
DR   EMBL; U66883; AAB53786.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   15 AA;  1808 MW;  1D1A4AB1EE1E3CFF CRC64;


  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     13 DRV 15


RESULT   7
Q9UWJ4
ID   Q9UWJ4      PRELIMINARY;      PRT;    16 AA.
AC   Q9UWJ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   SULFIDE DEHYDROGENASE ALPHA SUBUNIT (FRAGMENT).
OS   Pyrococcus furiosus.
OC   Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX   NCBI_TaxID=2261;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95050208; PubMed=7961401;
RA   Ma K., Adams M.W.;
RT   "Sulfide dehydrogenase from the hyperthermophilic archaeon Pyrococcus
RT   furiosus: a new multifunctional enzyme involved in the reduction of
RT   elemental sulfur.";
RL   J. Bacteriol. 176:6509-6517(1994).
SQ   SEQUENCE   16 AA;  1909 MW;  47EAAB14F8F6744A CRC64;


  Query Match             100.0%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      5 DRV 7


RESULT   8
O89807
ID   O89807      PRELIMINARY;      PRT;    17 AA.
AC   O89807;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LATE EXPRESSION FACTOR-1 (FRAGMENT).
GN   LEF-1.
OS   Epiphyas postvittana nucleopolyhedrovirus.
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC   Nucleopolyhedrovirus.
OX   NCBI_TaxID=70600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21342908; PubMed=11450943;
RA   Caradoc-Davies K.M., Graves S., O'Reilly D.R., Evans O.P., Ward V.K.;
RT   "Identification and in vivo characterization of the Epiphyas
RT   postvittana nucleopolyhedrovirus Ecdysteroid UDP-
RT   glucosyltransferase.";
RL   Virus Genes 22:255-264(2001).
DR   EMBL; AF052502; AAC34492.1; -.
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  2109 MW;  027F5F3CB5536F80 CRC64;


  Query Match             100.0%;  Score 15;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      9 DRV 11


RESULT   9
Q9BU72
ID   Q9BU72      PRELIMINARY;      PRT;    18 AA.
AC   Q9BU72;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 2.1 KDA PROTEIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=ENDOMETRIAL ADENOCARCINOMA;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002861; AAH02861.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   18 AA;  2064 MW;  371B21FD1E289B18 CRC64;


  Query Match             100.0%;  Score 15;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      8 DRV 10


RESULT  10
Q9UYK7
ID   Q9UYK7      PRELIMINARY;      PRT;    18 AA.
AC   Q9UYK7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   HYPOTHETICAL 2.1 KDA PROTEIN.
GN   PAB7382.
OS   Pyrococcus abyssi.
OC   Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX   NCBI_TaxID=29292;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ORSAY;
RA   Heilig R.;
RT   "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT   structure and evolution.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ248287; CAB50405.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   18 AA;  2105 MW;  B530635996611DCE CRC64;
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  Query Match             100.0%;  Score 15;  DB 17;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     11 DRV 13


RESULT  11
P83089
ID   P83089      PRELIMINARY;      PRT;    19 AA.
AC   P83089;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   25.3 KDA PROTEIN (FRAGMENT).
OS   Spinacia oleracea (Spinach).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE, AND SUBCELLULAR LOCATION.
RA   Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;
RL   Submitted (AUG-2001) to the SWISS-PROT data bank.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
KW   Chloroplast.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2093 MW;  EC33422F8633F1F9 CRC64;


  Query Match             100.0%;  Score 15;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     14 DRV 16


RESULT  12
Q9Z1I5
ID   Q9Z1I5      PRELIMINARY;      PRT;    19 AA.
AC   Q9Z1I5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CALCINEURIN A ALPHA (EC 3.1.3.16) (FRAGMENT).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=93111954; PubMed=1335233;
RA   Chang C., Takeda T., Mukai H., Shuntoh H., Kuno T., Tanaka C.;
RT   "Molecular cloning and characterization of the promoter region of the
RT   calcineurin A alpha gene.";
RL   Biochem. J. 288:801-805(1992).
DR   EMBL; D10480; BAA01283.1; -.
KW   Hydrolase.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2115 MW;  F905F8B134CCEC57 CRC64;


  Query Match             100.0%;  Score 15;  DB 11;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8.6e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     15 DRV 17


RESULT  13
Q9R519
ID   Q9R519      PRELIMINARY;      PRT;    20 AA.
AC   Q9R519;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   ISONICOTINATE DEHYDROGENASE (FRAGMENT).
OS   Mycobacterium.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae.
OX   NCBI_TaxID=1763;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94103749; PubMed=8277257;
RA   Kretzer A., Frunzke K., Andreesen J.R.;
RT   "Catabolism of isonicotinate by Mycobacterium sp. INA1: extended
RT   description of the pathway and purification of the molybdoenzyme
RT   isonicotinate dehydrogenase.";
RL   J. Gen. Microbiol. 139:2763-2772(1993).
SQ   SEQUENCE   20 AA;  2280 MW;  874DAA8637BB07C1 CRC64;


  Query Match             100.0%;  Score 15;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db      6 DRV 8


RESULT  14
Q9QVG0
ID   Q9QVG0      PRELIMINARY;      PRT;    20 AA.
AC   Q9QVG0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CLEAVED PROLACTIN-1, CLPRL-1=FRAGMENT A.
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92143803; PubMed=1736889;
RA   Andries M., Tilemans D., Denef C.;
RT   "Isolation of cleaved prolactin variants that stimulate DNA synthesis
RT   in specific cell types in rat pituitary cell aggregates in culture.";
RL   Biochem. J. 281:393-400(1992).
SQ   SEQUENCE   20 AA;  2146 MW;  89CA019A7668CBBA CRC64;


  Query Match             100.0%;  Score 15;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRV 3
          |||
Db     18 DRV 20


RESULT  15
Q47529
ID   Q47529      PRELIMINARY;      PRT;    22 AA.
AC   Q47529;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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DE HEMA PROTEIN.
GN HEMA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=93171869; PubMed=7679718;
RA Post D.A., Hore-Jensen B., Switzer R.L.;
RT "Characterization of the hemA-prs region of the Escherichia coli and
RT salmonella typhimurium chromosomes: identification of two open reading
RT frames and implications for prs expression.";
RL J. Gen. Microbiol. 139:259-266(1993).
DR EMBL; M77237; AAA24432.1; -.
SQ SEQUENCE 22 AA; 2340 MW; 25802412BB5B4E51 CRC64;

Query Match 100.0%; Score 15; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRV 3
|||
Db 10 DRV 12

Search completed: July 1, 2002, 07:45:17
Job time: 413 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:36:08 ; Search time 158.26 Seconds
(without alignments)
4.913 Million cell updates/sec

Title: US-09-723-197-4
Perfect score: 41
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 41 | 100.0 | 7 | 17 | AAR95665 | Angiotensin II fra |
| 2 | 41 | 100.0 | 7 | 19 | AAW65600 | Angiotensin II ana |
| 3 | 41 | 100.0 | 7 | 19 | AAW64731 | Angiotensin II pep |
| 4 | 41 | 100.0 | 7 | 19 | AAW71113 | Peptide AII(1-7) u |
| 5 | 41 | 100.0 | 7 | 20 | AAY49589 | Angiotensin analog |
| 6 | 41 | 100.0 | 7 | 20 | AAY50296 | Neutrophil-activat |
| 7 | 41 | 100.0 | 7 | 20 | AAY33904 | Angiotensin II ana |
| 8 | 41 | 100.0 | 7 | 20 | AAY30542 | Amino acid sequenc |
| 9 | 41 | 100.0 | 7 | 20 | AAY30586 | Amino acid sequenc |
| 10 | 41 | 100.0 | 7 | 20 | AAY32717 | Angiotensin II ana |
| 11 | 41 | 100.0 | 7 | 20 | AAY33771 | Angiotensin II (AI |
| 12 | 41 | 100.0 | 7 | 20 | AAY15348 | Angiotensin II (AI |
| 13 | 41 | 100.0 | 7 | 20 | AAY15308 | Angiotensin II (AI |
| 14 | 41 | 100.0 | 7 | 21 | AAB26205 | Anion exchange res |
| 15 | 41 | 100.0 | 7 | 21 | AAB27404 | Angiotensin II ana |
| 16 | 41 | 100.0 | 7 | 21 | AAB28102 | Angiotensin II ana |
| 17 | 41 | 100.0 | 7 | 21 | AAY84565 | Amino acid sequenc |
| 18 | 41 | 100.0 | 7 | 21 | AAY84127 | Peptide comprising |
| 19 | 41 | 100.0 | 7 | 21 | AAY77040 | Angiotensin II (AI |
| 20 | 41 | 100.0 | 7 | 21 | AAY57404 | Angiotensin peptid |
| 21 | 41 | 100.0 | 7 | 22 | AAE08874 | AII peptide (resid |
| 22 | 41 | 100.0 | 7 | 22 | AAE02991 | Human angiotensin |
| 23 | 41 | 100.0 | 7 | 22 | AAE03154 | Human angiotensin |
| 24 | 41 | 100.0 | 7 | 22 | AAB91463 | Angiotensin peptid |
| 25 | 41 | 100.0 | 8 | 6 | AAP50467 | Sequence of cyclop |
| 26 | 41 | 100.0 | 8 | 11 | AAR07584 | Hypotensive polype |
| 27 | 41 | 100.0 | 8 | 14 | AAR37433 | Promega peptide 8. |
| 28 | 41 | 100.0 | 8 | 16 | AAR83013 | Promega protein ki |
| 29 | 41 | 100.0 | 8 | 16 | AAR84269 | Angiotensin II dec |
| 30 | 41 | 100.0 | 8 | 17 | AAW65193 | Angiotensin II. S |
| 31 | 41 | 100.0 | 8 | 17 | AAR95662 | Angiotensin II. S |
| 32 | 41 | 100.0 | 8 | 18 | AAW33309 | Targetting conjuga |
| 33 | 41 | 100.0 | 8 | 18 | AAW32951 | Targetting conjuga |
| 34 | 41 | 100.0 | 8 | 18 | AAW11201 | Targetting conjuga |
| 35 | 41 | 100.0 | 8 | 18 | AAW14975 | Conjugating peptid |
| 36 | 41 | 100.0 | 8 | 18 | AAW09656 | Labelled peptide s |
| 37 | 41 | 100.0 | 8 | 18 | AAW19144 | Isoelectric point |
| 38 | 41 | 100.0 | 8 | 19 | AAW65596 | Angiotensin II. H |
| 39 | 41 | 100.0 | 8 | 19 | AAW65625 | Angiotensin II ana |
| 40 | 41 | 100.0 | 8 | 19 | AAW64763 | Angiotensin peptid |
| 41 | 41 | 100.0 | 8 | 19 | AAW64755 | Angiotensin II pep |
| 42 | 41 | 100.0 | 8 | 19 | AAW64758 | Angiotensin II pep |
| 43 | 41 | 100.0 | 8 | 19 | AAW64728 | Angiotensin II oct |
| 44 | 41 | 100.0 | 8 | 19 | AAW65628 | Angiotensin II ana |
| 45 | 41 | 100.0 | 8 | 19 | AAW71141 | Angiotensin II ana |

ALIGNMENTS

RESULT 1
AAR95665
ID AAR95665 standard; peptide; 7 AA.
XX
AC AAR95665;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(1-7).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 2
AAW65600
ID AAW65600 standard; peptide; 7 AA.
XX
AC AAW65600;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-7).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 3
AAW64731
ID AAW64731 standard; peptide; 7 AA.
XX
AC AAW64731;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #3.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in

CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 4
AAW71113
ID AAW71113 standard; peptide; 7 AA.
XX
AC AAW71113;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-7) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 5
AAY49589
ID AAY49589 standard; peptide; 7 AA.
XX
AC AAY49589;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:4.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIHP 7
          |||||||
Db      1 drvyihp 7
```

RESULT 6
AAY50296
ID AAY50296 standard; Peptide; 7 AA.
XX
AC AAY50296;
XX
DT 12-JAN-2000 (first entry)
XX
DE Neutrophil-activating pancreatic derived peptide 96.
XX
KW Cell activation; pancreas; treatment; cardiovascular disease; trauma;
KW inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;
KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;
KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;
KW trauma; protease inhibitor; hypertension; sepsis.
XX
OS Unidentified.
XX
PN WO9946367-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05247.
XX
PR 11-MAR-1998; 98US-0038894.
XX
PA (CELL-) CELL ACTIVATION INC.
PA (REGC ) UNIV CALIFORNIA.
PA (SCRI ) SCRIPPS RES INST.
XX
PI Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;
XX
DR WPI; 1999-580234/49.
XX
PT Use of cell activating compositions in developing products for
PT diagnosis and treatment of e.g. cardiovascular, inflammatory,
PT autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
PT diabetes, stroke or ischemia -
XX
PS Example 9; Page 184; 184pp; English.
XX
CC This invention describes a novel method for the use and preparation of
CC cell activating compositions which involves preparing a cell activating
CC composition comprising (a) homogenizing pancreatic tissue in buffer at
CC about neutral or higher pH to produce a homogenate; (b) removing
CC particulates from the homogenate; (c) optionally incubating the
CC resulting homogenate, with particulates removed, with a protease; and
CC (d) fractionating the homogenate and selecting fractions that exhibit
CC cell activation activity. The methods can be used for improving
CC treatment outcome or reducing risk of treatment of e.g. cardiovascular
CC disease, inflammatory disease, trauma, autoimmune diseases, arthritis,
CC organ rejection, diabetes and diabetic complications, stroke, ischemia,
CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic
CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.
CC They can be used in the veterinary treatment of a non-human subject.
CC Protease inhibitors can be used to lower cell activation resulting from
CC these diseases and deficiencies. The detection of an elevated level of
CC hydrogen peroxide can be used to detect an inflammatory condition. An
CC elevated level of hydrogen peroxide in plasma or whole blood and in the
CC presence of superoxide dismutase (SOD) indicates leukocyte up
CC regulation, e.g. indicative of the onset of an acute cardiovascular
CC disorders, such as disease onset or ischemic complications. An elevated
CC level of hydrogen peroxide in plasma or whole blood and a low level in
CC the presence of SOD is indicative of a chronic or immune compromised
CC condition e.g. hypertension or sepsis. AAY50201-Y50334 represent peptides
CC used in the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIHP 7
          |||||||
Db      1 drvyihp 7
```

RESULT 7
AAY33904
ID AAY33904 standard; peptide; 7 AA.
XX
AC AAY33904;
XX
DT 29-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-7).
XX
KW embryonic stem cell; ES; angiotensin; totipotent cell;
KW gene therapy; replacement therapy; angiotensin II; AII;
KW analogue.
XX
OS Homo sapiens.
XX
PN WO9942122-A1.
XX
PD 26-AUG-1999.
XX
PF 16-FEB-1999; 99WO-US03243.
XX
PR 19-FEB-1998; 98US-0075179.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527419/44.
XX
PT Promoting embryonal cell proliferation, using angiotensinogen and
PT angiotensin peptides, analogs or fragments
XX
PS Claim 2; Page 8; 76pp; English.
XX
CC This is the amino acid sequence of the Angiotensin II analogue,
CC AII(1-7). The formation of Angiotensin II (AII) is initiated by the
CC action of renin on the plasma substrate angiotensinogen.
CC This results in Angiotensin I (AI) which then converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY42372).
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC or AII AT2 type 2 receptor agonists can rapidly provide a large
CC population of ESCs (Embryonic Stem Cell) for use in replacement therapy.
CC Similarly, methods that increase in vivo proliferation of ESCs will
CC enhance the utility of replacement therapy by rapidly increasing local
CC concentration of the stem cells and their progeny at the site of
CC therapy. The method also increases the potential utility of ESCs as
CC vehicles for gene therapy in certain disorders by more efficiently
CC providing a large number of such cells for transfection, and also by
CC providing a more efficient means to rapidly expand transfected ESCs.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIHP 7
          |||||||
Db      1 drvyihp 7


RESULT   8
AAY30542
ID   AAY30542 standard; peptide; 7 AA.
XX
AC   AAY30542;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII1-7.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents  -
XX
PS   Claim 2; Page 52; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   7 AA;


  Query Match             100.0%;  Score 41;  DB 20;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 drvyihp 7


RESULT   9
AAY30586
ID   AAY30586 standard; peptide; 7 AA.
XX
AC   AAY30586;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII1-7.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
KW   gene therapy; hematopoietic disorder.
XX
OS   Synthetic.
XX
PN   WO9945945-A1.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05194.
XX
PR   10-MAR-1998;   98US-0077382.
PR   09-APR-1998;   98US-0081262.
PR   30-APR-1998;   98US-0083670.
PR   19-JUN-1998;   98US-0090096.
PR   22-JUN-1998;   98US-0090216.
PR   11-SEP-1998;   98US-0099957.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA   (RODG/) RODGERS K E.
PA   (DIZE/) DIZEREGA G.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551209/46.
XX
PT   Use of angiotensin and angiotensin type peptides, for mitigating
PT   radiation induced tissue damage, improving bone marrow transplantation
PT   and promoting megakaryocyte and platelet production  -
XX
PS   Claim 2; Page 85; 116pp; English.
XX
CC   AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes a method for mitigating
CC   radiation induced tissue damage, improving the effectiveness of
CC   radiation therapy, to support bone marrow transplantation, and
CC   promoting megakaryocyte production and mobilization and platelet
CC   production. The method comprises administration of the present peptides.
CC   The methods can be used to mitigate radiation induced tissue damage, to
CC   improve the effectiveness of radiation therapy, to support bone marrow
CC   transplantation, and to promote megakaryocyte production and
CC   mobilization and platelet production. They are used particularly in
CC   cancer therapy. They can also be used to provide megakaryocytes as
CC   vehicles for gene therapy in hematopoietic disorders, by providing a
CC   more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ   Sequence   7 AA;


  Query Match             100.0%;  Score 41;  DB 20;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 drvyihp 7


RESULT  10
AAY32717
ID   AAY32717 standard; peptide; 7 AA.
XX
AC   AAY32717;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Angiotensin II analogue AII(1-7).
XX
```

KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||||
Db 1 drvyihp 7

RESULT 11
AAY33771
ID AAY33771 standard; peptide; 7 AA.
XX
AC AAY33771;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(1-7).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US03772.
XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||||
Db 1 drvyihp 7

RESULT 12
AAY15348
ID AAY15348 standard; peptide; 7 AA.
XX
AC AAY15348;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-7).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX

DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX
PS Claim 2; Page 9; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 13
AAY15308
ID AAY15308 standard; peptide; 7 AA.
XX
AC AAY15308;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-7).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a
CC decapeptide called angiotensin I (AI) which is converted to AII by the
CC converting enzyme angiotensinase which removes the C-terminal His-Leu
CC residues from AI (AAY15339).
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 drvyihp 7

RESULT 14
AAB26205
ID AAB26205 standard; peptide; 7 AA.
XX
AC AAB26205;
XX
DT 23-FEB-2001 (first entry)
XX
DE Anion exchange resin EPM-1 test peptide #1.
XX
KW Anion exchange resin; ionic solute separation;
KW column liquid chromatography; EPM-1.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT /label= OTHER
FT /note= "modified by CONH2"
XX
PN WO200050465-A2.
XX
PD 31-AUG-2000.
XX
PF 23-FEB-2000; 2000WO-BR00023.
XX
PR 24-FEB-1999; 99BR-0004682.
XX
PA (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.
XX
PI Ryuichi Nakaie C, Cilli EM, Jabilut GN, Haddad Carvalho RS;
XX
DR WPI; 2000-572075/53.
XX
PT New crosslinked polystyrene containing aminomethyl groups, useful as
PT ion-exchange resin, particularly for separation of biomolecules from
PT electrophoretic gel
XX
PS Disclosure; Page 4; 17pp; English.
XX
CC The present sequence is a peptide used as a test for the novel anion
CC exchange resin aminomethyl-resin (EPM-1). The peptide has a charge of
CC plus 2 and so acts as a control for the occurrence of unspecific
CC interactions in the EPM-1 matrix. The EPM-1 resin can be used in column
CC liquid chromatography, in particular for the separation of ionic solutes.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIHP 7
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Db      1 drvyihp 7


RESULT  15
AAB27404
ID   AAB27404 standard; Peptide; 7 AA.
XX
AC   AAB27404;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Angiotensin II analog AII(1-7).
XX
KW   Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW   cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW   heart valve disease; myocarditis; angiotensin.
XX
OS   Synthetic.
XX
PN   WO200053211-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06198.
XX
PR   09-MAR-1999;   99US-0123678.
PR   31-AUG-1999;   99US-0151874.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-611400/58.
XX
PT   Promoting myocyte proliferation and myocardial tissue repair by
PT   contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT   for treating heart attacks, cardiomyopathies, inflammation and
PT   infection -
XX
PS   Claim 2; Page 10; 55pp; English.
XX
CC   The present invention relates to a method of promoting myocyte
CC   proliferation or differentiation by contacting myocytes with an active
CC   agent containing angiotensinogen, angiotensin I and II  (AI, AII), and
CC   angiotensin analogs. The present sequence is an angiotensin II analog
CC   of the invention. The active agents of the invention may be useful for
CC   promoting myocardial tissue repair following myocardial injury and for
CC   treating heart failure in a mammal. Administration to accelerate in
CC   vivo myocyte proliferation and/or to treat myocardial injuries can be
CC   used to treat cardiomyopathies, inflammation, infection, sepsis,
CC   ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC   ischemia and infarction and for improving cardiac output by increasing
CC   stroke volume.
XX
SQ   Sequence   7 AA;


  Query Match             100.0%;  Score 41;  DB 21;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
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Db      1 drvyihp 7


Search completed: July  1, 2002, 07:41:54
Job time: 346 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:37:59 ; Search time 59.1 Seconds
(without alignments)
2.893 Million cell updates/sec

Title: US-09-723-197-4
Perfect score: 41
Sequence: 1 DRVYIHP 7

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 41 | 100.0 | 7 | 2 | US-08-465-775-4 | Sequence 4, Appli |
| 2 | 41 | 100.0 | 7 | 3 | US-09-208-337-4 | Sequence 4, Appli |
| 3 | 41 | 100.0 | 7 | 3 | US-08-990-664-5 | Sequence 5, Appli |
| 4 | 41 | 100.0 | 7 | 4 | US-09-373-962-4 | Sequence 4, Appli |
| 5 | 41 | 100.0 | 7 | 4 | US-09-245-680-4 | Sequence 4, Appli |
| 6 | 41 | 100.0 | 7 | 4 | US-09-198-806C-4 | Sequence 4, Appli |
| 7 | 41 | 100.0 | 7 | 4 | US-09-352-191-4 | Sequence 4, Appli |
| 8 | 41 | 100.0 | 7 | 4 | US-09-012-400-4 | Sequence 4, Appli |
| 9 | 41 | 100.0 | 7 | 6 | 5451571-4 | Patent No. 5451571 |
| 10 | 41 | 100.0 | 8 | 1 | US-07-858-842-2 | Sequence 2, Appli |
| 11 | 41 | 100.0 | 8 | 1 | US-08-021-839A-3 | Sequence 3, Appli |
| 12 | 41 | 100.0 | 8 | 1 | US-08-184-935-2 | Sequence 2, Appli |
| 13 | 41 | 100.0 | 8 | 1 | US-08-212-433A-29 | Sequence 29, Appl |
| 14 | 41 | 100.0 | 8 | 1 | US-08-185-448-8 | Sequence 8, Appli |
| 15 | 41 | 100.0 | 8 | 1 | US-07-776-272-1 | Sequence 1, Appli |
| 16 | 41 | 100.0 | 8 | 1 | US-08-428-488-21 | Sequence 21, Appl |
| 17 | 41 | 100.0 | 8 | 1 | US-08-337-781-1 | Sequence 1, Appli |
| 18 | 41 | 100.0 | 8 | 1 | US-08-240-711-20 | Sequence 20, Appl |
| 19 | 41 | 100.0 | 8 | 1 | US-08-594-117-1 | Sequence 1, Appli |
| 20 | 41 | 100.0 | 8 | 1 | US-08-520-770-2 | Sequence 2, Appli |
| 21 | 41 | 100.0 | 8 | 1 | US-08-457-753-20 | Sequence 20, Appl |
| 22 | 41 | 100.0 | 8 | 2 | US-08-115-968-1 | Sequence 1, Appli |
| 23 | 41 | 100.0 | 8 | 2 | US-08-115-968-3 | Sequence 3, Appli |
| 24 | 41 | 100.0 | 8 | 2 | US-08-115-968-4 | Sequence 4, Appli |
| 25 | 41 | 100.0 | 8 | 2 | US-08-465-774-1 | Sequence 1, Appli |
| 26 | 41 | 100.0 | 8 | 2 | US-08-360-784B-2 | Sequence 2, Appli |
| 27 | 41 | 100.0 | 8 | 2 | US-08-623-833B-4 | Sequence 4, Appli |
| 28 | 41 | 100.0 | 8 | 2 | US-08-465-775-1 | Sequence 1, Appli |
| 29 | 41 | 100.0 | 8 | 2 | US-08-542-927-3 | Sequence 3, Appli |
| 30 | 41 | 100.0 | 8 | 3 | US-08-716-256-29 | Sequence 29, Appl |
| 31 | 41 | 100.0 | 8 | 3 | US-09-054-308A-2 | Sequence 2, Appli |
| 32 | 41 | 100.0 | 8 | 3 | US-09-280-047-7 | Sequence 7, Appli |
| 33 | 41 | 100.0 | 8 | 3 | US-09-208-337-1 | Sequence 1, Appli |
| 34 | 41 | 100.0 | 8 | 3 | US-08-990-664-1 | Sequence 1, Appli |
| 35 | 41 | 100.0 | 8 | 3 | US-08-990-664-30 | Sequence 30, Appl |
| 36 | 41 | 100.0 | 8 | 3 | US-08-927-128-16 | Sequence 16, Appl |
| 37 | 41 | 100.0 | 8 | 4 | US-09-210-249-1 | Sequence 1, Appli |
| 38 | 41 | 100.0 | 8 | 4 | US-09-210-249-8 | Sequence 8, Appli |
| 39 | 41 | 100.0 | 8 | 4 | US-09-373-962-1 | Sequence 1, Appli |
| 40 | 41 | 100.0 | 8 | 4 | US-09-373-962-29 | Sequence 29, Appl |
| 41 | 41 | 100.0 | 8 | 4 | US-09-373-962-32 | Sequence 32, Appl |
| 42 | 41 | 100.0 | 8 | 4 | US-09-373-962-42 | Sequence 42, Appl |
| 43 | 41 | 100.0 | 8 | 4 | US-09-289-693-25 | Sequence 25, Appl |
| 44 | 41 | 100.0 | 8 | 4 | US-09-245-680-1 | Sequence 1, Appli |
| 45 | 41 | 100.0 | 8 | 4 | US-09-245-680-29 | Sequence 29, Appl |

ALIGNMENTS

```
RESULT   1
US-08-465-775-4
; Sequence 4, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-4


  Query Match             100.0%;  Score 41;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
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Db       1 DRVYIHP 7
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RESULT   2
US-09-208-337-4
; Sequence 4, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-4


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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT   3
US-08-990-664-5
; Sequence 5, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-5


  Query Match             100.0%;  Score 41;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
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Db      1 DRVYIHP 7


RESULT   4
US-09-373-962-4
; Sequence 4, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-373-962-4


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Db      1 DRVYIHP 7
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US-09-245-680-4
; Sequence 4, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-245-680-4


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Qy      1 DRVYIHP 7
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; Sequence 4, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
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; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-198-806C-4


  Query Match           100.0%;  Score 41;  DB 4;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT   7
US-09-352-191-4
; Sequence 4, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-352-191-4


  Query Match           100.0%;  Score 41;  DB 4;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT   8
US-09-012-400-4
; Sequence 4, Application US/09012400D
; Patent No. 6335195
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
;  TITLE OF INVENTION: Proliferation and Differentiation
;  FILE REFERENCE: 97,017-G
;  CURRENT APPLICATION NUMBER: US/09/012,400D
;  CURRENT FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-7)
US-09-012-400-4


  Query Match           100.0%;  Score 41;  DB 4;  Length 7;
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Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT   9
5451571-4
;Patent No. 5451571
;    APPLICANT: FERRARIO, CARLOS M.;SANTOS, ROBSON A.S.;
;BROSNIHAN, KAY B.
;    TITLE OF INVENTION: PROCESS AND COMPOSITION FOR TREATING
;HYPERTENSION
;    NUMBER OF SEQUENCES: 5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/345,547
;      FILING DATE: 28-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 845,778
;      FILING DATE: 04-MAR-1992
;      APPLICATION NUMBER: 613,955
;      FILING DATE: 13-NOV-1990
;      APPLICATION NUMBER: 259,929
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;  FILING DATE: 19-OCT-1988
;SEQ ID NO:4:
;  LENGTH: 7
5451571-4

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Qy  1 DRVYIHP 7
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Db  1 DRVYIHP 7

RESULT 10
US-07-858-842-2
; Sequence 2, Application US/07858842
; Patent No. 5314807
; GENERAL INFORMATION:
;  APPLICANT: Yoshikawa, Masaaki
;  APPLICANT: Yokoyama, Keiichi
;  APPLICANT: Hasegawa, Masayasu
;  APPLICANT: Yasumoto, Ryouichi
;  APPLICANT: Fujita, Hiroyuki
;  TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN
;  NUMBER OF SEQUENCES: 5
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: ARMSTRONG & KUBOVCIK
;  STREET: 1725 K Street N.W. Suite 1000
;  CITY: Wasington
;  STATE: District of Columbia
;  COUNTRY: United States of America
;  ZIP: 20006
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/858,842
;  FILING DATE: 19920327
;  CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: JP 142283
;  FILING DATE: 29-MAR-1991
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: JP 298060
;  FILING DATE: 17-OCT-1991
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Gormley, Mary E.
;  REGISTRATION NUMBER: 34, 409
;  REFERENCE/DOCKET NUMBER: 920247
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (202) 659-2930
;  TELEFAX: (202) 887-0357
;  TELEX: 440142
; INFORMATION FOR SEQ ID NO: 2:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 8 amino acids
;  TYPE: AMINO ACID
;  TOPOLOGY: linear
;  MOLECULE TYPE: peptide
;  HYPOTHETICAL: NO
;  FRAGMENT TYPE: N-terminal
;  ORIGINAL SOURCE:
;  ORGANISM: Homo sapiens
US-07-858-842-2

  Query Match  100.0%;  Score 41;  DB 1;  Length 8;
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Qy  1 DRVYIHP 7
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Db  1 DRVYIHP 7

RESULT 11
US-08-021-839A-3
; Sequence 3, Application US/08021839A
; Patent No. 5326776
; GENERAL INFORMATION:
;  APPLICANT: Winn, Martin
;  APPLICANT: De, Biswanath
;  APPLICANT: Zydowsky, Thomas M.
;  APPLICANT: Kerkman, Daniel J.
;  APPLICANT: DeBernardis, John F.
;  APPLICANT: Rosenberg, Saul H.
;  APPLICANT: Shiosaki, Kazumi
;  APPLICANT: Basha, Fatima Z.
;  APPLICANT: Spina, Kenneth P.
;  APPLICANT: Von Geldern, Thomas W.
;  TITLE OF INVENTION: Angiotensin II Receptor Antagonists
;  NUMBER OF SEQUENCES: 4
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Edward H. Gorman, Jr.
;  STREET: Abbott Laboratories
;  STREET: D-377/AP6D
;  STREET: One Abbott Park Road
;  CITY: Abbott Park
;  STATE: Illinois
;  COUNTRY: USA
;  ZIP: 60064-3500
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette, 3.50 inch,800 Kb
;  COMPUTER: Apple Macintosh IIci
;  OPERATING SYSTEM: Macintosh
;  SOFTWARE: Microsoft Word 5.1
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/021,839A
;  FILING DATE: 24-FEB-1993
;  CLASSIFICATION: 514
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 07/844,817
;  FILING DATE: 02-MAR-1992
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Steven R. Crowley
;  REGISTRATION NUMBER: 31,604
;  REFERENCE/DOCKET NUMBER: 5136.US.P1
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (708) 938-7742
;  TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 3:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 8 amino acid residues
;  TYPE: amino acid
;  TOPOLOGY: unknown
;  MOLECULE TYPE:
;  DESCRIPTION: peptide
US-08-021-839A-3

  Query Match  100.0%;  Score 41;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches  7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 DRVYIHP 7
      |||||||
Db  1 DRVYIHP 7

RESULT 12
US-08-184-935-2
; Sequence 2, Application US/08184935

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; Patent No. 5476770
;  GENERAL INFORMATION:
;    APPLICANT:  PRADELLES, PHILIPPE
;    TITLE OF INVENTION:  IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
;    TITLE OF INVENTION:  OR HAPTEN
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,935
;      FILING DATE:  24-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5476770man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  846-286-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-184-935-2


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Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT  13
US-08-212-433A-29
; Sequence 29, Application US/08212433A
; Patent No. 5538897
;  GENERAL INFORMATION:
;    APPLICANT:  Yates, III, John R.
;    APPLICANT:  Eng, James K.
;    TITLE OF INVENTION:  USE OF MASS SPECTROMETRY FRAGMENTATION
;    TITLE OF INVENTION:  PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
;    TITLE OF INVENTION:  DATABASES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart St. Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/212,433A
;      FILING DATE:  14-MAR-1994
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hughes, Richard L.
;      REGISTRATION NUMBER:  31,264
;      REFERENCE/DOCKET NUMBER:  16336-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-467-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-212-433A-29


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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT  14
US-08-185-448-8
; Sequence 8, Application US/08185448
; Patent No. 5580747
;  GENERAL INFORMATION:
;    APPLICANT:  SHULTZ, JOHN W.
;    APPLICANT:  WHITE, DOUGLAS H.
;    TITLE OF INVENTION:  NON-RADIOACTIVE KINASE,
;    TITLE OF INVENTION:  PHOSPHATASE AND PROTEASE ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDRUS, SCEALES, STARKE & SAWALL
;      STREET:  100 E. WISCONSIN AVENUE, SUITE 1100
;      CITY:  MILWAUKEE
;      STATE:  WISCONSIN
;      COUNTRY:  USA
;      ZIP:  53202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version
;      SOFTWARE:  #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/185,448
;      FILING DATE:  21-JAN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/791,928
;      FILING DATE:  12-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SARA, CHARLES S
;      REGISTRATION NUMBER:  30492
;      REFERENCE/DOCKET NUMBER:  F.3347-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 255-2022
;      TELEFAX:  (608) 255-2182
;      TELEX:  26832 ANDSTARK
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
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;    FEATURE:
;      NAME/KEY:  Binding-site
;      LOCATION:  1
;      OTHER INFORMATION:  /label= LABEL
;      OTHER INFORMATION:  /note= "LOCATION OF LISSAMINE RHODAMINE
;      OTHER INFORMATION:  DETECTION TAG"
US-08-185-448-8


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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


RESULT  15
US-07-776-272-1
;Sequence 1, Application US/07776272
; Patent No. 5612454
;  GENERAL INFORMATION:
;    APPLICANT:  Kaminuma, Toshihiko
;    APPLICANT:  Iida, Toshii
;    APPLICANT:  Tajima, Masahiro
;    TITLE OF INVENTION:  Process for Purification of Polypeptide
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wegner, Cantor, Mueller & Player
;      STREET:  1233 20th St. N.W.  P.O. Box 18218
;      CITY:  Washington
;      STATE:  District of Columbia
;      COUNTRY:  United States of America
;      ZIP:  20036-8218
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/776,272
;      FILING DATE:  19911129
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Player, William E
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  P-450-23167
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-0400
;      TELEFAX:  202-887-0605
;      TELEX:  440706
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
US-07-776-272-1


  Query Match             100.0%;  Score 41;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db      1 DRVYIHP 7


Search completed: July  1, 2002, 07:43:00
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:38:24 ; Search time 122.73 Seconds
(without alignments)
9.867 Million cell updates/sec

Title: US-09-723-197-4
Perfect score: 41
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 41 | 100.0 | 14 | 5 | Q10757 | Q10757 theromyzon |
| 2 | 41 | 100.0 | 245 | 6 | Q95J13 | Q95j13 pan troglod |
| 3 | 41 | 100.0 | 295 | 4 | Q9HA44 | Q9ha44 homo sapien |
| 4 | 41 | 100.0 | 461 | 11 | Q9D2V0 | Q9d2v0 mus musculu |
| 5 | 41 | 100.0 | 477 | 4 | Q96FD5 | Q96fd5 homo sapien |
| 6 | 41 | 100.0 | 485 | 4 | Q96F91 | Q96f91 homo sapien |
| 7 | 41 | 100.0 | 485 | 6 | Q9GLP7 | Q9glp7 pan troglod |
| 8 | 41 | 100.0 | 485 | 6 | Q9GLP6 | Q9glp6 gorilla gor |
| 9 | 41 | 100.0 | 485 | 6 | Q9GLN8 | Q9gln8 pan troglod |
| 10 | 41 | 100.0 | 486 | 6 | Q9TSZ0 | Q9tsz0 callithrix |
| 11 | 40 | 97.6 | 10 | 13 | Q9PS07 | Q9ps07 alligator m |
| 12 | 38 | 92.7 | 171 | 17 | Q971G2 | Q971g2 sulfolobus |
| 13 | 36 | 87.8 | 277 | 10 | O80539 | O80539 arabidopsis |
| 14 | 36 | 87.8 | 280 | 10 | Q940A3 | Q940a3 arabidopsis |
| 15 | 36 | 87.8 | 289 | 10 | Q9FVU1 | Q9fvu1 arabidopsis |
| 16 | 35 | 85.4 | 436 | 11 | Q9CSJ0 | Q9csj0 mus musculu |
| 17 | 35 | 85.4 | 533 | 4 | Q96SF7 | Q96sf7 homo sapien |
| 18 | 35 | 85.4 | 694 | 2 | Q9EWA5 | Q9ewa5 streptomyce |
| 19 | 35 | 85.4 | 1094 | 2 | Q93H78 | Q93h78 streptomyce |
| 20 | 35 | 85.4 | 1147 | 5 | Q9Y1H3 | Q9y1h3 dictyosteli |
| 21 | 34 | 82.9 | 128 | 16 | Q9K1A7 | Q9k1a7 neisseria m |
| 22 | 34 | 82.9 | 132 | 16 | Q9PG09 | Q9pg09 xylella fas |
| 23 | 34 | 82.9 | 149 | 2 | Q57032 | Q57032 synechocyst |
| 24 | 34 | 82.9 | 168 | 8 | O48244 | O48244 dennyus car |
| 25 | 34 | 82.9 | 168 | 8 | O48245 | O48245 dennyus car |
| 26 | 34 | 82.9 | 175 | 5 | Q9GQE4 | Q9gqe4 branchiosto |
| 27 | 34 | 82.9 | 183 | 5 | Q9GQE6 | Q9gqe6 branchiosto |
| 28 | 34 | 82.9 | 316 | 2 | Q9Z5B8 | Q9z5b8 streptomyce |
| 29 | 34 | 82.9 | 380 | 8 | Q9G0M4 | Q9g0m4 arapaima gi |
| 30 | 34 | 82.9 | 624 | 5 | Q966R5 | Q966r5 branchiosto |
| 31 | 34 | 82.9 | 883 | 5 | Q9XYX1 | Q9xyx1 drosophila |
| 32 | 33 | 80.5 | 56 | 16 | Q9PCT3 | Q9pct3 xylella fas |
| 33 | 33 | 80.5 | 87 | 10 | Q93YL0 | Q93yl0 brassica na |
| 34 | 33 | 80.5 | 88 | 10 | Q93YM2 | Q93ym2 brassica ju |
| 35 | 33 | 80.5 | 221 | 10 | Q9ZVR9 | Q9zvr9 arabidopsis |
| 36 | 33 | 80.5 | 237 | 4 | Q9H5S9 | Q9h5s9 homo sapien |
| 37 | 33 | 80.5 | 249 | 13 | Q9W7Q1 | Q9w7q1 paralichthy |
| 38 | 33 | 80.5 | 275 | 4 | Q9BTA8 | Q9bta8 homo sapien |
| 39 | 33 | 80.5 | 288 | 2 | Q55040 | Q55040 synechococc |
| 40 | 33 | 80.5 | 380 | 8 | Q955N7 | Q955n7 siphateles |
| 41 | 33 | 80.5 | 394 | 5 | P91817 | P91817 tachypleus |
| 42 | 33 | 80.5 | 437 | 13 | Q9DDU4 | Q9ddu4 brachydanio |
| 43 | 33 | 80.5 | 457 | 6 | Q9XSH5 | Q9xsh5 saimiri bol |
| 44 | 33 | 80.5 | 695 | 5 | Q9XUQ0 | Q9xuq0 caenorhabdi |
| 45 | 33 | 80.5 | 736 | 10 | Q9LMH6 | Q9lmh6 arabidopsis |

ALIGNMENTS

RESULT 1
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7

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Db      1 DRVYIHP 7


RESULT   2
Q95J13
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AC   Q95J13;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (FRAGMENT).
GN   REN.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=504, AND 505;
RA   Satta Y.;
RT   "Comparison of DNA and protein polymorphims between humans and
RT   chimpanzees.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062027; BAB55856.1; -.
DR   EMBL; AB062028; BAB55857.1; -.
FT   NON_TER     245    245
SQ   SEQUENCE   245 AA;  26317 MW;  E0092390B9803E0B CRC64;


  Query Match             100.0%;  Score 41;  DB 6;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     34 DRVYIHP 40


RESULT   3
Q9HA44
ID   Q9HA44      PRELIMINARY;      PRT;   295 AA.
AC   Q9HA44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE   TRANSCRIPTION FACTOR TBX6.
GN   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022330; BAB14014.1; -.
DR   HSSP; P24781; 1XBR.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33197 MW;  F2BD3E53E0ED21E0 CRC64;


  Query Match             100.0%;  Score 41;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db    170 DRVYIHP 176


RESULT   4
Q9D2V0
ID   Q9D2V0      PRELIMINARY;      PRT;   461 AA.
AC   Q9D2V0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018763; BAB31393.1; -.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
SQ   SEQUENCE   461 AA;  50327 MW;  446EB0881079251F CRC64;


  Query Match             100.0%;  Score 41;  DB 11;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     30 DRVYIHP 36


RESULT   5
Q96FD5
ID   Q96FD5      PRELIMINARY;      PRT;   477 AA.
AC   Q96FD5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
```

```
DE   SIMILAR TO ANGIOTENSINOGEN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011231; AAH11231.1; -.
SQ   SEQUENCE   477 AA;  51985 MW;  AB79B8B70592FDE2 CRC64;


  Query Match             100.0%;  Score 41;  DB 4;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     25 DRVYIHP 31


RESULT   6
Q96F91
ID   Q96F91      PRELIMINARY;      PRT;   485 AA.
AC   Q96F91;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN (SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE
DE   A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 8).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011519; AAH11519.1; -.
SQ   SEQUENCE   485 AA;  53114 MW;  50BA5E9DCD4C8E7F CRC64;


  Query Match             100.0%;  Score 41;  DB 4;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     34 DRVYIHP 40


RESULT   7
Q9GLP7
ID   Q9GLP7      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188487; AAG29056.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53140 MW;  49EFB54AF31F8ADC CRC64;


  Query Match             100.0%;  Score 41;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     34 DRVYIHP 40


RESULT   8
Q9GLP6
ID   Q9GLP6      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLP6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shattuck-Eidens D., McGrail M., Stone S.;
RT   "Germline mutations in the angiotensinogen gene cause predisposition
RT   to type 1 diabetes mellitus.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF188488; AAG29057.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53186 MW;  53BC9235271C8255 CRC64;


  Query Match             100.0%;  Score 41;  DB 6;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |||||||
Db     34 DRVYIHP 40


RESULT   9
Q9GLN8
ID   Q9GLN8      PRELIMINARY;      PRT;   485 AA.
AC   Q9GLN8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN.
GN   AGT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20469400; PubMed=11013071;
RA   Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA   Jeunemaitre X.;
RT   "Human-Chimpanzee DNA sequence variation in the four major genes of
RT   the renin angiotensin system.";
RL   Genomics 69:14-26(2000).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AF193461; AAG30306.1; -.
DR   EMBL; AF193458; AAG30306.1; JOINED.
DR   EMBL; AF193459; AAG30306.1; JOINED.
DR   EMBL; AF193460; AAG30306.1; JOINED.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin.
SQ   SEQUENCE   485 AA;  53110 MW;  C14C67E49A53F05F CRC64;
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Query Match 100.0%; Score 41; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIHP 7
           |||||||
Db      34 DRVYIHP 40
```

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RESULT  10
Q9TSZ0
ID   Q9TSZ0      PRELIMINARY;      PRT;   486 AA.
AC   Q9TSZ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR.
GN   ANGT.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065005; PubMed=10598135;
RA   Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;
RT   "Cloning and characterization of marmoset renin: comparison with human
RT   renin.";
RL   J. Cardiovasc. Pharmacol. 34:893-897(1999).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   EMBL; AJ132343; CAB64880.1; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW   Serpin; Signal.
FT   SIGNAL       1     33       POTENTIAL.
FT   CHAIN       34    486       ANGIOTENSINOGEN.
SQ   SEQUENCE   486 AA;  53374 MW;  5408129B2F71FB8B CRC64;
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Query Match 100.0%; Score 41; DB 6; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIHP 7
           |||||||
Db      34 DRVYIHP 40
```

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RESULT  11
Q9PS07
ID   Q9PS07      PRELIMINARY;      PRT;    10 AA.
AC   Q9PS07;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ANGIOTENSIN I, ANG I.
OS   Alligator mississippiensis (American alligator).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX   NCBI_TaxID=8496;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93307610; PubMed=8319878;
RA   Takei Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA   Stephens G.A., Sakakibara S.;
RT   "New angiotensin I isolated from a reptile, Alligator
RT   mississippiensis.";
RL   Gen. Comp. Endocrinol. 90:214-219(1993).
SQ   SEQUENCE   10 AA;  1216 MW;  CEE38DD761F2DB42 CRC64;
```

Query Match 97.6%; Score 40; DB 13; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.08;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIHP 7
           ||||:||
Db       1 DRVYVHP 7
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RESULT  12
Q971G2
ID   Q971G2      PRELIMINARY;      PRT;   171 AA.
AC   Q971G2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN ST1391.
GN   ST1391.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000986; BAB66458.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   171 AA;  18700 MW;  897F397EAD34EF0A CRC64;
```

Query Match 92.7%; Score 38; DB 17; Length 171;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIHP 7
           |:|||||
Db      16 DKVYIHP 22
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RESULT  13
O80539
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ID   O80539      PRELIMINARY;      PRT;   277 AA.
AC   O80539;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   F14J9.24 PROTEIN.
GN   F14J9.24.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
RA   Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
RA   Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S.,
RA   Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC003970; AAC33217.1; -.
SQ   SEQUENCE   277 AA;  31908 MW;  EB65DCCA29C36D46 CRC64;

  Query Match             87.8%;  Score 36;  DB 10;  Length 277;
  Best Local Similarity   71.4%;  Pred. No. 16;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |:||:||
Db    108 DKVYLHP 114


RESULT  14
Q940A3
ID   Q940A3      PRELIMINARY;      PRT;   280 AA.
AC   Q940A3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 32.4 KDA PROTEIN.
GN   F14J9.24.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA   Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA   Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RT   "Full Length cDNA of gene F14J9.24 (GI:3482932).";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY056149; AAL07228.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   280 AA;  32441 MW;  4252585A11002102 CRC64;

  Query Match             87.8%;  Score 36;  DB 10;  Length 280;
  Best Local Similarity   71.4%;  Pred. No. 17;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |:||:||
Db    119 DKVYLHP 125


RESULT  15
Q9FVU1
ID   Q9FVU1      PRELIMINARY;      PRT;   289 AA.
AC   Q9FVU1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   HYPOTHETICAL 33.2 KDA PROTEIN.
GN   T8L23.8.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
DR   EMBL; AC079733; AAG50752.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   289 AA;  33181 MW;  BE15FFAB7CD7C608 CRC64;

  Query Match             87.8%;  Score 36;  DB 10;  Length 289;
  Best Local Similarity   71.4%;  Pred. No. 17;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          |:||:||
Db    111 DKVYLHP 117


Search completed: July  1, 2002, 07:45:10
Job time: 406 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:38:59 ; Search time 69.93 Seconds
(without alignments)
9.619 Million cell updates/sec

Title: US-09-723-197-4
Perfect score: 41
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 41 | 100.0 | 10 | 2 | S65432 | angiotensin I - ho |
| 2 | 41 | 100.0 | 14 | 2 | A01250 | angiotensin precur |
| 3 | 41 | 100.0 | 15 | 2 | A60834 | angiotensin I prec |
| 4 | 41 | 100.0 | 476 | 1 | JC2318 | angiotensin precur |
| 5 | 41 | 100.0 | 477 | 1 | ANRT | angiotensin precur |
| 6 | 41 | 100.0 | 477 | 1 | A29978 | angiotensin precur |
| 7 | 41 | 100.0 | 485 | 1 | ANHU | angiotensin precur |
| 8 | 41 | 100.0 | 540 | 2 | S72233 | transcription fact |
| 9 | 40 | 97.6 | 10 | 2 | A60624 | angiotensin I - Ja |
| 10 | 40 | 97.6 | 10 | 2 | A90917 | angiotensin precur |
| 11 | 40 | 97.6 | 10 | 2 | A90345 | angiotensin precur |
| 12 | 39 | 95.1 | 11 | 2 | S07207 | Crinia-angiotensin |
| 13 | 37 | 90.2 | 625 | 1 | TBBO | thrombin (EC 3.4.2 |
| 14 | 36 | 87.8 | 277 | 2 | E86229 | hypothetical prote |
| 15 | 36 | 87.8 | 289 | 2 | C96610 | hypothetical prote |
| 16 | 35 | 85.4 | 305 | 2 | D69362 | tRNA intron endonu |
| 17 | 35 | 85.4 | 1355 | 1 | VGBEI1 | 149K glycoprotein |
| 18 | 34 | 82.9 | 128 | 2 | G81220 | hypothetical prote |
| 19 | 34 | 82.9 | 132 | 2 | F82800 | hypothetical prote |
| 20 | 34 | 82.9 | 316 | 2 | T34838 | probable transfera |
| 21 | 34 | 82.9 | 481 | 2 | S76115 | hypothetical prote |
| 22 | 33 | 80.5 | 56 | 2 | H82647 | hypothetical prote |
| 23 | 33 | 80.5 | 178 | 2 | B42845 | 3-hydroxybutyrate |
| 24 | 33 | 80.5 | 221 | 2 | A86163 | protein F15K9.22 [ |
| 25 | 33 | 80.5 | 559 | 2 | AI2227 | hypothetical prote |
| 26 | 33 | 80.5 | 617 | 2 | S10511 | thrombin (EC 3.4.2 |
| 27 | 33 | 80.5 | 622 | 1 | TBHU | thrombin (EC 3.4.2 |
| 28 | 33 | 80.5 | 681 | 2 | I78558 | hypothetical Brach |
| 29 | 33 | 80.5 | 695 | 1 | S05008 | complement subcomp |
| 30 | 33 | 80.5 | 695 | 2 | T24950 | hypothetical prote |
| 31 | 33 | 80.5 | 736 | 2 | D86271 | protein F16A14.2 [ |
| 32 | 33 | 80.5 | 1062 | 2 | H83966 | carbamoyl-phosphat |
| 33 | 33 | 80.5 | 1063 | 2 | T46284 | hypothetical prote |
| 34 | 33 | 80.5 | 1071 | 2 | F39845 | carbamoyl-phosphat |
| 35 | 33 | 80.5 | 1076 | 2 | A69409 | carbamoyl-phosphat |
| 36 | 33 | 80.5 | 1095 | 2 | T13964 | probable histone d |
| 37 | 33 | 80.5 | 3971 | 2 | T44806 | mycosubtilin synth |
| 38 | 32 | 78.0 | 105 | 1 | FETWT | ferredoxin [3Fe-4S |
| 39 | 32 | 78.0 | 177 | 2 | C71329 | hypothetical prote |
| 40 | 32 | 78.0 | 223 | 2 | AG1166 | Ribulose-5-Phospha |
| 41 | 32 | 78.0 | 230 | 2 | E69233 | carbamoyl-phosphat |
| 42 | 32 | 78.0 | 263 | 2 | F84339 | hypothetical prote |
| 43 | 32 | 78.0 | 301 | 2 | D64938 | hypothetical prote |
| 44 | 32 | 78.0 | 301 | 2 | A99940 | hypothetical prote |
| 45 | 32 | 78.0 | 301 | 2 | E85788 | hypothetical prote |

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||||
Db 1 DRVYIHP 7

RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 41; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||||
Db 1 DRVYIHP 7

RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 1 DRVYIHP 7

RESULT 4
JC2318
angiotensin precursor - sheep
N;Alternate names: angiotensinogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC2318; A25406
R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
A;Reference number: JC2318; MUID:95072318
A;Accession: JC2318
A;Molecule type: mRNA
A;Residues: 1-476 <NAG>
A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 465 as Leu
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Aust. J. Biochem. 154, 597-601, 1986
A;Title: Purification and characterization of ovine angiotensinogen.
A;Reference number: A25406; MUID:86136099
A;Accession: A25406
A;Molecule type: protein
A;Residues: 25-37,'X',39 <FER>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-476/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin #status predicted <MAT>
F;295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 41; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 25 DRVYIHP 31

RESULT 5
ANRT

angiotensin precursor - rat
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849
A;Accession: A93945
A;Molecule type: mRNA
A;Residues: 1-477 <OHK>
A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, char
A;Reference number: A90456; MUID:82091819
A;Accession: A90456
A;Molecule type: protein
A;Residues: 25-41 <BOU>
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin I #status experimental <PP1>
F;25-32/Product: angiotensin II #status experimental <PP2>
F;26-32/Product: angiotensin III #status experimental <PP3>
F;295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 41; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
||||||| 
Db 25 DRVYIHP 31

RESULT 6
A29978
angiotensin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29978
R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A;Title: Molecular cloning of the mouse angiotensinogen gene.
A;Reference number: A29978; MUID:88284703
A;Accession: A29978
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-477 <CLO>
A;Cross-references: GB:AF045887; GB:J03046; NID:g2842773; PIDN:AAC01765.1; PID:g28427
C;Genetics:
A;Introns: 277/1; 366/2; 414/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MAT>

Query Match 100.0%; Score 41; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7

```
          |||||||
Db      25 DRVYIHP 31


RESULT   7
ANHU
angiotensin precursor [validated] - human
N;Alternate names: angiotensinogen
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1982 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C;Accession: A35203; A31362; I37168; I37169; A60825; I39462; A90487; A90226; I54281; A01
R;Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,
J. Biol. Chem. 265, 7576-7582, 1990
A;Title: Structure and expression of the human angiotensinogen gene. Identification of a
A;Reference number: A35203; MUID:90237063
A;Accession: A35203
A;Molecule type: DNA
A;Residues: 1-485 <FUK>
A;Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
A;Gaillard, I.; Clauser, E.; Corvol, P.
DNA 8, 87-99, 1989
A;Title: Structure of human angiotensinogen gene.
A;Reference number: A31362; MUID:89170129
A;Accession: A31362
A;Molecule type: DNA
A;Residues: 1-267,'M',269-332,'E',334-485 <GAI>
A;Cross-references: GB:M24686; GB:M24687; GB:M24688
A;Note: the authors translated the codon GAA for residue 333 as Gln
R;Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.
J. Biol. Chem. 269, 28598-28605, 1994
A;Title: Identification of cell type-dependent enhancer core element located in the 3'-d
A;Reference number: I37168; MUID:95050659
A;Accession: I37168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <NIB1>
A;Cross-references: EMBL:X15324; NID:g1197496; PIDN:CAA33385.1; PID:g1197497
A;Accession: I37169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 287-375 <NIB2>
A;Cross-references: EMBL:X15325; NID:g28695
R;Kunapuli, S.P.; Benedict, C.R.; Kumar, A.
Arch. Biochem. Biophys. 254, 642-646, 1987
A;Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.
A;Reference number: A60825; MUID:87212053
A;Accession: A60825
A;Molecule type: mRNA
A;Residues: 32-184 <KUN1>
R;Kunapuli, S.P.; Kumar, A.
Circ. Res. 60, 786-790, 1987
A;Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence o
A;Reference number: I39462; MUID:87244745
A;Accession: I39462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-338 <KUN2>
A;Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181
R;Kageyama, R.; Ohkubo, H.; Nakanishi, S.
Biochemistry 23, 3603-3609, 1984
A;Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ
A;Reference number: A90487; MUID:85000455
A;Accession: A90487
A;Molecule type: mRNA
A;Residues: 1-267,'M',269-485 <KAG>
A;Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640
A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
R;Tewksbury, D.A.; Dart, R.A.; Travis, J.
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
A;Title: The amino terminal amino acid sequence of human angiotensinogen.
A;Reference number: A90226; MUID:81255848
A;Accession: A90226
A;Molecule type: protein
A;Residues: 34-46,'X',48-50,'S',52-57,'D' <TEW>
R;Hixson, J.E.; Powers, P.K.
Hum. Genet. 96, 110-112, 1995
A;Title: Detection and characterization of new mutations in the human angiotensinogen
A;Reference number: I54281; MUID:95331754
A;Accession: I54281
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 176-241,'I',243-267,'M',269-287,'ANLSAG' <HIX>
A;Cross-references: GB:S78529; NID:g999316; PIDN:AAD14287.1; PID:g4261987
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C;Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,
o induces thirst.
C;Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
C;Genetics:
A;Gene: GDB:AGT
A;Cross-references: GDB:118750; OMIM:106150
A;Map position: 1q42-1q43
A;Introns: 286/1; 375/2; 423/3
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>
F;34-485/Product: angiotensinogen #status predicted <MPT>
F;34-43/Product: angiotensin I #status experimental <PP1>
F;34-41/Product: angiotensin II #status experimental <PP2>
F;35-41/Product: angiotensin III #status experimental <PP3>
F;47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 41;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db      34 DRVYIHP 40


RESULT   8
S72233
transcription factor tbx6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S72233; S72232
R;Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.
submitted to the EMBL Data Library, May 1996
A;Reference number: S72233
A;Accession: S72233
A;Molecule type: mRNA
A;Residues: 1-540 <AGU>
A;Cross-references: EMBL:U57331; NID:g1620601; PIDN:AAC53110.1; PID:g1620602
R;Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B
Genetics 144, 249-254, 1996
A;Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.
A;Reference number: S72230; MUID:97032942
A;Accession: S72232
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 100-280 <AGW>
A;Cross-references: EMBL:U57331
C;Genetics:
A;Gene: tbx6
C;Superfamily: T-box homology
C;Keywords: DNA binding
F;100-282/Domain: T-box homology <TBX>


  Query Match             100.0%;  Score 41;  DB 2;  Length 540;
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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIHP 7
          |||||||
Db    170 DRVYIHP 176
```

RESULT 9
A60624
angiotensin I - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of thes
A;Reference number: A60624; MUID:90284684
A;Accession: A60624
A;Molecule type: protein
A;Residues: 1-10 <TAK>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.6%; Score 40; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.045;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7
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RESULT 10
A90917
angiotensin precursor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90917; A01250
R;Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A;Reference number: A90917; MUID:74127845
A;Accession: A90917
A;Molecule type: protein
A;Residues: 1-10 <NAK>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.6%; Score 40; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.045;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7
```

RESULT 11
A90345
angiotensin precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A90345; A01250
R;Elliott, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A;Title: The amino acid sequence in a hypertensin.
A;Reference number: A90345
A;Accession: A90345
A;Molecule type: protein
A;Residues: 1-10 <ELL>
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.6%; Score 40; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.045;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7
```

RESULT 12
S07207
Crinia-angiotensin, skin - frog (Crinia georgiana)
C;Species: Crinia georgiana
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C;Accession: S07207
R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A;Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II
A;Reference number: S07207; MUID:80024575
A;Accession: S07207
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides

Query Match 95.1%; Score 39; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 0.079;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYIHP 7
          ||:|:||
Db      4 DRIYVHP 10
```

RESULT 13
TBBO
thrombin (EC 3.4.21.5) precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
C;Accession: S02537; A00915; A37552; I46045; S67518
R;Irwin, D.M.; Robertson, K.A.; MacGillivray, R.T.A.
J. Mol. Biol. 200, 31-45, 1988
A;Title: Structure and evolution of the bovine prothrombin gene.
A;Reference number: S02537; MUID:88245190
A;Accession: S02537
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-625 <IRW>
R;MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A;Title: Characterization of bovine prothrombin mRNA and its translation product.
A;Reference number: A00915; MUID:84203525
A;Accession: A00915
A;Molecule type: mRNA
A;Residues: 1-230,'H',232-625 <MAC>
A;Note: 600-Asn was also found
R;Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
in Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C.,
A;Reference number: A37552
A;Accession: A37552
A;Molecule type: protein
A;Residues: 44-287,'N',289-352,'E',354,'Q',356-548,'ND',551-599,'N',601-625 <MAG>
A;Note: the evidence for 231-Ser is strong
A;Note: disulfide bonds and carbohydrate binding sites were determined
R;Park, C.H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
A;Title: Three-dimensional structure of the kringle sequence: structure of prothrombi

A;Reference number: A37553; MUID:86296631
A;Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R;Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A;Title: Characterization of the bovine prothrombin gene.
A;Reference number: A37554; MUID:86077733
A;Contents: annotation; gene structure
R;MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A;Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A;Reference number: I46045; MUID:81054926
A;Accession: I46045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 466-599,'N',601-625 <MA2>
A;Cross-references: EMBL:V00135; NID:g772; PIDN:CAA23451.1; PID:g808945
R;Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A;Title: Identification of the proteolytic thrombin fragments formed after cleavage with
A;Reference number: S67518; MUID:95154277
A;Accession: S67518
A;Status: preliminary
A;Molecule type: protein
A;Residues: 318-325;333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibri
C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
tivation peptide and cleaves the remaining part into light and heavy chains. The activat
.
C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombin,
C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C;Comment: The prothrombin precursor is synthesized in the liver.
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; glyco
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-43/Domain: propeptide #status predicted <PRO>
F;28-88/Domain: Gla domain homology <GLA>
F;44-625/Product: prothrombin #status experimental <MPT>
F;44-199/Domain: activation peptide 1 #status experimental <FR1>
F;109-187/Domain: kringle homology <KR1>
F;200-317/Domain: activation peptide 2 #status experimental <FR2>
F;214-292/Domain: kringle homology <KR2>
F;318-366/Product: thrombin light chain #status experimental <LCH>
F;367-625/Product: thrombin heavy chain #status experimental <HCH>
F;367-616/Domain: trypsin homology <TRY>
F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;61-66,91-104,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-553,5
120,144,419/Binding site: carbohydrate (Asn) (covalent) #status experimental
409,465,571/Active site: His, Asp, Ser #status experimental

  Query Match 90.2%; Score 37; DB 1; Length 625;
  Best Local Similarity 71.4%; Pred. No. 16;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|::||||
Db 448 DKIYIHP 454

RESULT 14
E86229
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86229
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: E86229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <STO>
A;Cross-references: GB:AE005172; NID:g3482932; PIDN:AAC33217.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match 87.8%; Score 36; DB 2; Length 277;
  Best Local Similarity 71.4%; Pred. No. 11;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|:||:||
Db 108 DKVYLHP 114

RESULT 15
C96610
hypothetical protein T8L23.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96610
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: C96610
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <STO>
A;Cross-references: GB:AE005173; NID:g11055863; PIDN:AAG28331.1; GSPDB:GN00141
C;Genetics:
A;Gene: T8L23.8
A;Map position: 1

  Query Match 87.8%; Score 36; DB 2; Length 289;
  Best Local Similarity 71.4%; Pred. No. 11;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|:||:||
Db 111 DKVYLHP 117

Search completed: July 1, 2002, 07:46:27
Job time: 448 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 07:39:14 ; Search time 34.05 Seconds
(without alignments)
7.960 Million cell updates/sec

Title: US-09-723-197-4
Perfect score: 41
Sequence: 1 DRVYIHP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 41 | 100.0 | 8 | 1 | ANG2_BOTJA | Q10582 bothrops ja |
| 2 | 41 | 100.0 | 14 | 1 | ANGT_HORSE | P01016 equus cabal |
| 3 | 41 | 100.0 | 436 | 1 | TBX6_HUMAN | O95947 homo sapien |
| 4 | 41 | 100.0 | 476 | 1 | ANGT_SHEEP | P20757 ovis aries |
| 5 | 41 | 100.0 | 477 | 1 | ANGT_MOUSE | P11859 mus musculu |
| 6 | 41 | 100.0 | 477 | 1 | ANGT_RAT | P01015 rattus norv |
| 7 | 41 | 100.0 | 485 | 1 | ANGT_HUMAN | P01019 homo sapien |
| 8 | 41 | 100.0 | 540 | 1 | TBX6_MOUSE | P70327 mus musculu |
| 9 | 40 | 97.6 | 10 | 1 | ANG1_BOTJA | Q10581 bothrops ja |
| 10 | 40 | 97.6 | 10 | 1 | ANGT_BOVIN | P01017 bos taurus |
| 11 | 40 | 97.6 | 10 | 1 | ANGT_CHICK | P01018 gallus gall |
| 12 | 39 | 95.1 | 11 | 1 | ANGT_CRIGE | P09037 crinia geor |
| 13 | 37 | 90.2 | 625 | 1 | THRB_BOVIN | P00735 bos taurus |
| 14 | 35 | 85.4 | 305 | 1 | ENDA_ARCFU | O29362 archaeoglob |
| 15 | 35 | 85.4 | 501 | 1 | TX18_HUMAN | O95935 homo sapien |
| 16 | 35 | 85.4 | 602 | 1 | TX15_MOUSE | O70306 mus musculu |
| 17 | 35 | 85.4 | 613 | 1 | TX18_MOUSE | Q9epz6 mus musculu |
| 18 | 35 | 85.4 | 1355 | 1 | VG46_HSVI1 | Q00104 ictalurid h |
| 19 | 34 | 82.9 | 481 | 1 | Y335_SYNY3 | Q55587 synechocyst |
| 20 | 34 | 82.9 | 3110 | 1 | LMA2_HUMAN | P24043 homo sapien |
| 21 | 33 | 80.5 | 178 | 1 | BDH_BOVIN | Q02337 bos taurus |
| 22 | 33 | 80.5 | 528 | 1 | GD_DROME | O62589 drosophila |
| 23 | 33 | 80.5 | 617 | 1 | THRB_RAT | P18292 rattus norv |
| 24 | 33 | 80.5 | 622 | 1 | THRB_HUMAN | P00734 homo sapien |
| 25 | 33 | 80.5 | 681 | 1 | TBR1_MOUSE | Q64336 mus musculu |
| 26 | 33 | 80.5 | 682 | 1 | TBR1_HUMAN | Q16650 homo sapien |
| 27 | 33 | 80.5 | 695 | 1 | CASP_MESAU | P15156 mesocricetu |
| 28 | 33 | 80.5 | 1071 | 1 | CARB_BACSU | P25994 bacillus su |
| 29 | 33 | 80.5 | 1149 | 1 | HDA6_MOUSE | Q9z2v5 mus musculu |
| 30 | 33 | 80.5 | 1215 | 1 | HDA6_HUMAN | Q9ubn7 homo sapien |
| 31 | 32 | 78.0 | 78 | 1 | FER_THETH | P03942 thermus aqu |
| 32 | 32 | 78.0 | 177 | 1 | Y404_TREPA | O83419 treponema p |
| 33 | 32 | 78.0 | 294 | 1 | UP08_ECOLI | P39173 escherichia |
| 34 | 32 | 78.0 | 378 | 1 | EXT1_CAEEL | O01704 caenorhabdi |
| 35 | 32 | 78.0 | 414 | 1 | TBX3_CHICK | O73718 gallus gall |
| 36 | 32 | 78.0 | 427 | 1 | AROA_AERPE | Q9yek9 aeropyrum p |
| 37 | 32 | 78.0 | 482 | 1 | NCAP_CCHFV | P27317 crimean-con |
| 38 | 32 | 78.0 | 485 | 1 | NCAP_HAZVJ | P27318 hazara viru |
| 39 | 32 | 78.0 | 535 | 1 | TX21_HUMAN | Q9ul17 homo sapien |
| 40 | 32 | 78.0 | 618 | 1 | THRB_MOUSE | P19221 mus musculu |
| 41 | 32 | 78.0 | 692 | 1 | EOMD_XENLA | P79944 xenopus lae |
| 42 | 32 | 78.0 | 701 | 1 | TBX2_MOUSE | Q60707 mus musculu |
| 43 | 32 | 78.0 | 702 | 1 | TBX2_HUMAN | Q13207 homo sapien |
| 44 | 32 | 78.0 | 721 | 1 | NICA_CAEEL | Q23316 caenorhabdi |
| 45 | 32 | 78.0 | 742 | 1 | TBX3_HUMAN | O15119 homo sapien |

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 41; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHP 7
|||||||
Db 1 DRVYIHP 7

RESULT 2
ANGT_HORSE
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a polypeptide renin substrate.";

```
RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.022;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db       1 DRVYIHP 7


RESULT   3
TBX6_HUMAN
ID   TBX6_HUMAN     STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
RN   [2]
     SEQUENCE OF 135-272 FROM N.A.
     TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db     170 DRVYIHP 176


RESULT   4
ANGT_SHEEP
ID   ANGT_SHEEP     STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    476       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 0.79;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db      25 DRVYIHP 31


RESULT   5
ANGT_MOUSE
ID   ANGT_MOUSE     STANDARD;      PRT;   477 AA.
AC   P11859;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88284703; PubMed=3397061;
RA   Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT   "Molecular cloning of the mouse angiotensinogen gene.";
RL   Genomics 2:240-248(1988).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AF045887; AAC01765.1; -.
DR   EMBL; AF045886; AAC01765.1; JOINED.
DR   EMBL; AF045885; AAC01765.1; JOINED.
DR   EMBL; AF045884; AAC01765.1; JOINED.
DR   PIR; A29978; A29978.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51990 MW;  A877F4029F338607 CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 0.79;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db      25 DRVYIHP 31


RESULT   6
ANGT_RAT
ID   ANGT_RAT       STANDARD;      PRT;   477 AA.
AC   P01015;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR;
RX   MEDLINE=83169849; PubMed=6572971;
RA   Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA   Nakanishi S.;
RT   "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN   [2]
RP   SEQUENCE OF 25-34.
RX   MEDLINE=73060322; PubMed=4344907;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. II. Structure of rat
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 20:1579-1581(1972).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; L00094; AAA98779.1; -.
DR   EMBL; L00091; AAA98779.1; JOINED.
DR   EMBL; L00092; AAA98779.1; JOINED.
DR   EMBL; L00093; AAA98779.1; JOINED.
DR   PIR; A01251; ANRT.
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DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51981 MW;  689051A5788D693D CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 0.79;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

      1 DRVYIHP 7
        |||||||
Db     25 DRVYIHP 31


RESULT   7
ANGT_HUMAN
ID   ANGT_HUMAN     STANDARD;      PRT;   485 AA.
AC   P01019; Q16358; Q16359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
GN   SERPINA8 OR AGT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89170129; PubMed=2924688;
RA   Gaillard I., Clauser E., Corvol P.;
RT   "Structure of human angiotensinogen gene.";
RL   DNA 8:87-99(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85000455; PubMed=6089875;
RA   Kageyama R., Ohkubo H., Nakanishi S.;
RT   "Primary structure of human preangiotensinogen deduced from the
RT   cloned cDNA sequence.";
RL   Biochemistry 23:3603-3609(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90237063; PubMed=1692023;
RA   Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA   Murakami K.;
RT   "Structure and expression of the human angiotensinogen gene.
RT   Identification of a unique and highly active promoter.";
RL   J. Biol. Chem. 265:7576-7582(1990).
RN   [4]
RP   SEQUENCE OF 1-338 FROM N.A.
RX   MEDLINE=87244745; PubMed=2885106;
RA   Kunapuli S.P., Kumar A.;
RT   "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT   presence of its mRNA in rat heart.";
RL   Circ. Res. 60:786-790(1987).
RN   [5]
RP   SEQUENCE OF 34-45, AND SUBUNITS.
RC   TISSUE=Serum;
RX   MEDLINE=95293954; PubMed=7539791;
RA   Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA   Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT   "Identification of angiotensinogen and complement C3dg as novel
RT   proteins binding the proform of eosinophil major basic protein in
RT   human pregnancy serum and plasma.";
RL   J. Biol. Chem. 270:13645-13651(1995).
RN   [6]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=69014170; PubMed=4300938;
RA   Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT   "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL   Biochim. Biophys. Acta 168:106-112(1968).
RN   [7]
RP   STRUCTURE BY NMR OF ANGIOTENSIN II.
RX   MEDLINE=98151281; PubMed=9492317;
RA   Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT   "The octapeptide angiotensin II adopts a well-defined structure in a
RT   phospholipid environment.";
RL   Eur. J. Biochem. 251:448-453(1998).
RN   [8]
RP   VARIANTS MET-207; THR-268 AND CYS-281.
RX   MEDLINE=93008239; PubMed=1394429;
RA   Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA   Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA   Lalouel J.-M., Corvol P.;
RT   "Molecular basis of human hypertension: role of angiotensinogen.";
RL   Cell 71:169-180(1992).
RN   [9]
RP   VARIANT THR-268.
RX   MEDLINE=93291876; PubMed=8513325;
RA   Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA   Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
RA   Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT   "A molecular variant of angiotensinogen associated with
RT   preeclampsia.";
RL   Nat. Genet. 4:59-61(1993).
RN   [10]
RP   VARIANTS ILE-242; ARG-244 AND CYS-281.
RX   MEDLINE=95331754; PubMed=7607642;
RA   Hixson J.E., Powers P.K.;
RT   "Detection and characterization of new mutations in the human
RT   angiotensinogen gene (AGT).";
RL   Hum. Genet. 96:110-112(1995).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
CC       heterotetramer with the proform of PRG2 and as a complex (probably
CC       a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
CC       ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
CC       (PIH) (PREECLAMPSIA).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02215; AAA51731.1; -.
DR   EMBL; M24689; AAA51679.1; -.
DR   EMBL; M24686; AAA51679.1; JOINED.
DR   EMBL; M24687; AAA51679.1; JOINED.
DR   EMBL; M24688; AAA51679.1; JOINED.
DR   EMBL; X15324; CAA33385.1; -.
DR   EMBL; X15325; CAA33385.1; JOINED.
DR   EMBL; X15326; CAA33385.1; JOINED.
DR   EMBL; X15327; CAA33385.1; JOINED.
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DR   EMBL; M69110; AAA52282.1; -.
DR   EMBL; S78529; AAD14287.1; -.
DR   EMBL; S78530; AAD14288.1; -.
DR   PIR; A01249; ANHU.
DR   PIR; A31362; A31362.
DR   PIR; A35203; A35203.
DR   SWISS-2DPAGE; P01019; HUMAN.
DR   MIM; 106150; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW   Disease mutation; Polymorphism.
FT   SIGNAL       1     33
FT   CHAIN       34    485       ANGIOTENSINOGEN.
FT   PEPTIDE     34     43       ANGIOTENSIN I.
FT   PEPTIDE     34     41       ANGIOTENSIN II.
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    207    207       T -> M.
FT                               /FTId=VAR_007093.
FT   VARIANT    242    242       T -> I (IN HYPERTENSION).
FT                               /FTId=VAR_007094.
FT   VARIANT    244    244       L -> R (IN HYPERTENSION).
FT                               /FTId=VAR_007095.
FT   VARIANT    268    268       M -> T (IN HYPERTENSION).
FT                               /FTId=VAR_007096.
FT   VARIANT    281    281       Y -> C (IN HYPERTENSION).
FT                               /FTId=VAR_007097.
FT   CONFLICT   333    333       Q -> E (IN REF. 1).
SQ   SEQUENCE   485 AA;  53154 MW;  5026C2DFB2DD236E CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 0.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db      34 DRVYIHP 40


RESULT   8
TBX6_MOUSE
ID   TBX6_MOUSE     STANDARD;      PRT;   540 AA.
AC   P70327;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX6 (T-box protein 6).
GN   TBX6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97032942; PubMed=8878690;
RA   Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA   Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT   "Evolution of mouse T-box genes by tandem duplication and cluster
RT   dispersion.";
RL   Genetics 144:249-254(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastrula;
RX   MEDLINE=97115702; PubMed=8954725;
RA   Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT   "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT   gastrulation.";
RL   Dev. Biol. 180:534-542(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=98140705; PubMed=9490412;
RA   Chapman D.L., Papaioannou V.E.;
RT   "Three neural tubes in mouse embryos with mutations in the T-box gene
RT   Tbx6.";
RL   Nature 391:695-697(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC       MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC       DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC       PATHWAY.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC       STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC       MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC       PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC       AS THE SOURCE OF MESODERM.
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U57331; AAC53110.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:102539; Tbx6.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       61     64       POLY-ALA.
FT   DOMAIN       79     82       POLY-PRO.
FT   DNA_BIND    100    273       T-BOX.
SQ   SEQUENCE   540 AA;  58628 MW;  BC834CE2745E8E61 CRC64;


  Query Match             100.0%;  Score 41;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 0.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |||||||
Db     170 DRVYIHP 176


RESULT   9
ANG1_BOTJA
ID   ANG1_BOTJA     STANDARD;      PRT;    10 AA.
AC   Q10581;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Angiotensin-like peptide I (Fragment).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
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```
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=96208932; PubMed=8829801;
RA   Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT   "Isolation and identification of angiotensin-like peptides from the
RT   plasma of the snake Bothrops jararaca.";
RL   Comp. Biochem. Physiol. 113B:467-473(1996).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1308 MW;  CEF50DD761F2DB42 CRC64;


  Query Match             97.6%;  Score 40;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 0.025;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7


RESULT  10
ANGT_BOVIN
ID   ANGT_BOVIN     STANDARD;      PRT;    10 AA.
AC   P01017;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RA   Elliott D.F., Peart W.S.;
RT   "The amino acid sequence in a hypertensin.";
RL   Biochem. J. 65:246-254(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90345; A90345.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1282 MW;  CEEFBDD761F2DB42 CRC64;


  Query Match             97.6%;  Score 40;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 0.025;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7


RESULT  11
ANGT_CHICK
ID   ANGT_CHICK     STANDARD;      PRT;    10 AA.
AC   P01018;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
GN   SERPINA8 OR AGT.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken;
RX   MEDLINE=74127845; PubMed=4361802;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. 3. Structure of fowl
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 21:2085-2087(1973).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=90284684; PubMed=2191893;
RA   Takei Y., Hasegawa Y.;
RT   "Vasopressor and depressor effects of native angiotensins and
RT   inhibition of these effects in the Japanese quail.";
RL   Gen. Comp. Endocrinol. 79:12-22(1990).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   PIR; A90917; A90917.
DR   PIR; A60624; A60624.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1232 MW;  CEFBEDD761F2DB42 CRC64;


  Query Match             97.6%;  Score 40;  DB 1;  Length 10;
  Best Local Similarity   85.7%;  Pred. No. 0.025;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYIHP 7
          ||||:||
Db      1 DRVYVHP 7


RESULT  12
ANGT_CRIGE
ID   ANGT_CRIGE     STANDARD;      PRT;    11 AA.
AC   P09037;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Crinia-angiotensin II.
OS   Crinia georgiana (Quacking frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Crinia.
OX   NCBI_TaxID=8374;
RN   [1]
RP   SEQUENCE.
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RC   TISSUE=Skin;
RX   MEDLINE=80024575; PubMed=488254;
RA   Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT   "Amino acid composition and sequence of crinia-angiotensin, an
RT   angiotensin II-like endecapeptide from the skin of the Australian
RT   frog Crinia georgiana.";
RL   Experientia 35:1132-1133(1979).
DR   PIR; S07207; S07207.
KW   Vasoconstrictor.
SQ   SEQUENCE   11 AA;  1271 MW;  8A0921F7DB50440A CRC64;


  Query Match             95.1%;  Score 39;  DB 1;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 0.044;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           ||:|:|| 
Db       4 DRIYVHP 10


RESULT  13
THRB_BOVIN
ID   THRB_BOVIN     STANDARD;      PRT;   625 AA.
AC   P00735;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Prothrombin precursor (EC 3.4.21.5).
GN   F2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88245190; PubMed=3379642;
RA   Irwin D.M., Robertson K.A., Macgillivray R.T.A.;
RT   "Structure and evolution of the bovine prothrombin gene.";
RL   J. Mol. Biol. 200:31-45(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84203525; PubMed=6326805;
RA   McGillivray R.T.A., Davie E.W.;
RT   "Characterization of bovine prothrombin mRNA and its translation
RT   product.";
RL   Biochemistry 23:1626-1634(1984).
RN   [3]
RP   SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA   Magnusson S., Sottrup-Jensen L., Petersen T.E., Claeys H.;
RL   (In) Hemker H.C., Veltkamp J.J. (eds.);
RL   Boerhaave symposium on prothrombin and related coagulation factors,
RL   pp.25-46, Leiden University Press, Leiden (1975).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX   MEDLINE=86296631; PubMed=3741841;
RA   Park C.H., Tulinsky A.;
RT   "Three-dimensional structure of the kringle sequence: structure of
RT   prothrombin fragment 1.";
RL   Biochemistry 25:3977-3982(1986).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX   MEDLINE=91311686; PubMed=1856869;
RA   Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
RT   "Structure of bovine prothrombin fragment 1 refined at 2.25-A
RT   resolution.";
RL   J. Mol. Biol. 220:481-494(1991).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
RX   MEDLINE=92190185; PubMed=1547238;
RA   Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
RT   "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
RT   prothrombin fragment 1.";
RL   Biochemistry 31:2554-2566(1992).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX   MEDLINE=92218459; PubMed=1560020;
RA   Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT   "The structure of residues 7-16 of the A alpha-chain of human
RT   fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL   J. Biol. Chem. 267:7911-7920(1992).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX   MEDLINE=92389319; PubMed=1518046;
RA   Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
RA   Martin P.D., Edwards B.F.P., Bode W.;
RT   "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
RT   formed with the benzamidine and arginine-based thrombin inhibitors
RT   NAPAP, 4-TAPAP and MQPA. A starting point for improving
RT   antithrombotics.";
RL   J. Mol. Biol. 226:1085-1089(1992).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
RX   MEDLINE=97102783; PubMed=8947023;
RA   van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
RA   Hoffken W., Huber R.;
RT   "The ornithodorin-thrombin crystal structure, a key to the TAP
RT   enigma?";
RL   EMBO J. 15:6011-6017(1996).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
RX   MEDLINE=98004486; PubMed=9342325;
RA   Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
RA   Huber R., Bode W.;
RT   "Structure of the thrombin complex with triabin, a lipocalin-like
RT   exosite-binding inhibitor derived from a triatomine bug.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
RN   [11]
RP   GENE STRUCTURE.
RX   MEDLINE=86077733; PubMed=3000440;
RA   Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
RT   "Characterization of the bovine prothrombin gene.";
RL   Biochemistry 24:6854-6861(1985).
CC   -!- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC       FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC       AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
CC   -!- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC       RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC       ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC       ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC       CHARGED PHOSPHOLIPID SURFACE,WHICH IS ESSENTIAL FOR THE CONVERSION
CC       OF PROTHROMBIN TO THROMBIN.
CC   -!- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC       PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC       FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC       THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC       HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC       V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC       THROMBIN.
CC   -!- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC       FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC       BY FACTOR XA.
CC   -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
CC   -!- DATABASE: NAME=ProZyme technical fact sheet;
CC       WWW="http://www.prozyme.com/technical/thrombindata.html".
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; V00135; CAA23451.1; -.
DR   EMBL; J00041; AAA30781.1; -.
DR   PIR; A00915; TBBO.
DR   PIR; S02537; S02537.
DR   PDB; 1BBR; 31-JAN-94.
DR   PDB; 1ETR; 31-JAN-94.
DR   PDB; 1ETS; 31-JAN-94.
DR   PDB; 1ETT; 31-JAN-94.
DR   PDB; 1HRT; 31-JAN-94.
DR   PDB; 2PF1; 31-JAN-94.
DR   PDB; 2PF2; 31-JAN-94.
DR   PDB; 2SPT; 31-MAY-94.
DR   PDB; 1MKW; 07-JUL-97.
DR   PDB; 1MKX; 07-JUL-97.
DR   PDB; 1TBQ; 14-OCT-96.
DR   PDB; 1TBR; 14-OCT-96.
DR   PDB; 1TOC; 23-JUL-97.
DR   PDB; 1VIT; 21-APR-97.
DR   PDB; 1YCP; 06-MAY-98.
DR   PDB; 1A0H; 17-JUN-98.
DR   PDB; 1AVG; 16-FEB-99.
DR   MEROPS; S01.217; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003966; Prothrombin.
DR   InterPro; IPR001254; Trypsin.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00051; kringle; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00001; GLABLOOD.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00130; KR; 2.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS00021; KRINGLE_1; 2.
DR   PROSITE; PS50070; KRINGLE_2; 2.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
     Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
     Hydrolase; Serine protease; Kringle; Signal; 3D-structure.
FT   SIGNAL       1     24       POTENTIAL.
FT   PROPEP      25     43
FT   CHAIN       44    625       PROTHROMBIN.
FT   PEPTIDE     44    199       ACTIVATION PEPTIDE (FRAGMENT 1).
FT   PEPTIDE    200    317       ACTIVATION PEPTIDE (FRAGMENT 2).
FT   CHAIN      318    366       THROMBIN LIGHT CHAIN (A).
FT   CHAIN      367    625       THROMBIN HEAVY CHAIN (B).
FT   DOMAIN     109    187       KRINGLE 1.
FT   DOMAIN     214    292       KRINGLE 2.
FT   DOMAIN     367    625       SERINE PROTEASE.
FT   SITE       199    200       CLEAVAGE (BY THROMBIN).
FT   SITE       317    318       CLEAVAGE (BY FACTOR XA).
FT   SITE       366    367       CLEAVAGE (BY FACTOR XA).
FT   ACT_SITE   409    409       CHARGE RELAY SYSTEM.
FT   ACT_SITE   465    465       CHARGE RELAY SYSTEM.
FT   ACT_SITE   571    571       CHARGE RELAY SYSTEM.
FT   MOD_RES     50     50       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     51     51       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     58     58       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     60     60       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     63     63       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     64     64       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     69     69       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     70     70       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     73     73       GAMMA-CARBOXYGLUTAMIC ACID.
FT   MOD_RES     76     76       GAMMA-CARBOXYGLUTAMIC ACID.
FT   CARBOHYD   120    120       N-LINKED (GLCNAC. . .).

  Query Match             90.2%;  Score 37;  DB 1;  Length 625;
  Best Local Similarity   71.4%;  Pred. No. 6.4;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYIHP 7
           |::|||| 
Db     448 DKIYIHP 454


RESULT  14
ENDA_ARCFU
ID   ENDA_ARCFU     STANDARD;      PRT;   305 AA.
AC   O29362;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative tRNA-intron endonuclease (EC 3.1.27.9).
GN   ENDA OR AF0900.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC   Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- FUNCTION: CLEAVES PRE-TRNA AT THE 5' AND 3' SPLICE SITES TO
CC       RELEASE THE INTRON. THE PRODUCTS ARE AN INTRON AND TWO TRNA HALF-
CC       MOLECULES BEARING 2',3' CYCLIC PHOSPHATE AND 5'-OH TERMINI (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of pre-tRNA,
CC       producing 5'-hydroxyl and 2',3'-cyclic phosphate termini, and
CC       specifically removing the intron.
CC   -!- SIMILARITY: BELONGS TO THE TRNA-INTRON ENDONUCLEASE FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE001041; AAB90338.1; -.
DR   HSSP; Q58819; 1A79.
DR   TIGR; AF0900; -.
DR   InterPro; IPR002827; tRNA_int_endo.
DR   Pfam; PF01974; tRNA_int_endo; 1.
DR   Pfam; PF02778; tRNA_int_endo_N; 1.
KW   Hydrolase; Nuclease; Endonuclease; tRNA processing; Complete proteome.
SQ   SEQUENCE   305 AA;  35959 MW;  DC0B5A5DEBD99E35 CRC64;


  Query Match             85.4%;  Score 35;  DB 1;  Length 305;
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Best Local Similarity 57.1%; Pred. No. 7.7;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 DRVYIHP 7
             |::|:||
Db      26 DKIYLHP 32
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RESULT  15
TX18_HUMAN
ID   TX18_HUMAN     STANDARD;      PRT;   501 AA.
AC   O95935; Q9UJI6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T-box transcription factor TBX18 (T-box protein 18) (Fragment).
GN   TBX18.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bates K.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 42-223 FROM N.A.
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL035694; CAB45196.1; -.
DR   EMBL; AJ010278; CAB37937.1; -.
DR   HSSP; P24781; 1XBR.
DR   MIM; 604613; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   NON_TER       1      1
FT   DNA_BIND     42    224       T-BOX.
SQ   SEQUENCE   501 AA;  54229 MW;  45A732B009A4E5F5 CRC64;
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Query Match 85.4%; Score 35; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 RVYIHP 7
             ||||||
Db     115 RVYIHP 120
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Search completed: July 1, 2002, 07:47:07
Job time: 473 sec

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